SEQUENCE LISTING

<110> Jones, Brian E.
       Kolkman, Marc
       Leeflang, Chris
       Oh, Hiroshi
       Poulose, A.J.
       Sadlowski, Eugene S.
       Shaw, Andrew
       van der Kleij, Wilhelmus A.H.
       van Marrenwijk, Leo

<120> Serine Proteases, Nucleic Acids Encoding Serine Enzymes and
       Vectors and Host Cells Incorporating Same

<130> GC819-2-US/B

<140> US 10/576,331
<141> 2004-11-19

<150> PCT/US2004/039066
<151> 2004-11-19

<150> US 60/523,609
<151> 2003-11-19

<160> 656

<170> PatentIn version 3.2

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<213> Cellulomonas strain 69B4

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cgtcgtcgtc gccgtcaagg ccggagccca ggacgtcgcc gccggcctcg tcgaaggtgc   660
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caaccccacc gggaccttcg ccgggtccag cttcccgggc aacgactacg cgttcgtccg   900
taccggggcc ggcgtgaacc tgctggccca ggtcaacaac tactccggtg gccgcgtcca   960
ggtcgccggg cacaccgcgg cccccgtcgg ctcggccgtg tgccggtccg ggtcgaccac   1020
cgggtggcac tgcggcacca tcactgcgct caactcctcg gtcacctacc ccgagggcac   1080
cgtccgcggc ctgatccgca ccaccgtctg cgccgagccc ggcgactccg gtggctcgct   1140
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tggcaccacg ttcttccagc cggtcaaccc catcctccag gcgtacggcc tgaggatgat    1320
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ccacgcctgg ccgagaagct cgaccccgac ctcctcgagg ccatggagcg cgacctgggc    180
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gccctcgagg ccacgacga cgtgcccacc tggtacgtcg acgtcccgac caacagcgtc    480
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cccaccggga ccttcgccgg gtccagcttc ccgggcaacg actacgcgtt cgtccgtacc    780
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gccgggcaca ccgcggcccc cgtcggctcg gccgtgtgcc ggtccgggtc gaccaccggg    900
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<212>   DNA
<213>   Cellulomonas spp.

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accctggcgt tccagcacga cgcagccgag accggcgagg ccctcgccga agagctcgac    180
gaggacttcg ccggcacctg ggtcgaggac gacgtcctgt acgtcgccac caccgacgag    240
gacgccgtcg aggaggtcga gggcgaaggc ccacggccg tcaccgtcga gcactccctg    300
gccgacctcg aggcctggaa gaccgtcctc gacgccgccc tcgagggcca cgacgacgtg    360
cccacctggt acgtcgacgt cccgaccaac agcgtcgtcg tcgccgtcaa ggccggagcc    420
caggacgtcg ccgccggcct cgtcgaaggt gccgacgtcc cgtccgacgc cgtgaccttc    480
gtcgagaccg acgagacccc gcggaccatg ttcgacgtga tcggcggcaa cgcctacacc    540
atcgggggggc gcagccgctg ctcgatcggg ttcgcggtca cggcgggtt catcaccgcc    600
ggccactgcg gccgcaccgg cgccaccacc gccaacccca ccgggacctt cgccgggtcc    660
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agcttcccgg gcaacgacta cgcgttcgtc cgtaccgggg ccggcgtgaa cctgctggcc        720
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tgcgccgagc ccggcgactc cggtggctcg ctgctcgccg gcaaccaggc ccagggcgtc        960
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<212>    DNA
<213>    Cellulomonas spp.


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gccaacccca ccgggacctt cgccgggtcc agcttcccgg gcaacgacta cgcgttcgtc        180
cgtaccgggg ccggcgtgaa cctgctggcc caggtcaaca actactccgg tggccgcgtc        240
caggtcgccg ggcacaccgc ggcccccgtc ggctcggccg tgtgccggtc cgggtcgacc        300
accgggtggc actgcggcac catcactgcg ctcaactcct cggtcaccta ccccgagggc        360
accgtccgcg gcctgatccg caccaccgtc tgcgccgagc ccggcgactc cggtggctcg        420
ctgctcgccg gcaaccaggc ccagggcgtc acgtccggcg gctccggcaa ctgccgcacc        480
ggtggcacca cgttcttcca gccggtcaac cccatcctcc aggcgtacgg cctgaggatg        540
atcaccacgg actcgggcag cagcccg                                            567


<210>    5
<211>    83
<212>    DNA
<213>    Cellulomonas strain 69B4


<400>    5
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caggcggcat ggccgcccag gcc                                                83


<210>    6
<211>    495
<212>    PRT
<213>    Cellulomonas strain 69B4


<400>    6


Met Thr Pro Arg Thr Val Thr Arg Ala Leu Ala Val Ala Thr Ala Ala
1               5                   10                  15
Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala Asn Glu Pro Ala
            20                  25                  30
Pro Pro Gly Ser Ala Ser Ala Pro Pro Arg Leu Ala Glu Lys Leu Asp
        35                  40                  45
Pro Asp Leu Leu Glu Ala Met Glu Arg Asp Leu Gly Leu Asp Ala Glu
    50                  55                  60
Glu Ala Ala Ala Thr Leu Ala Phe Gln His Asp Ala Ala Glu Thr Gly
65                  70                  75                  80
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Glu Ala Leu Ala Glu Glu Leu Asp Glu Asp Phe Ala Gly Thr Trp Val
             85                  90                  95
Glu Asp Asp Val Leu Tyr Val Ala Thr Thr Asp Glu Asp Ala Val Glu
            100                 105                 110
Glu Val Glu Gly Glu Gly Ala Thr Ala Val Thr Val Glu His Ser Leu
            115                 120                 125
Ala Asp Leu Glu Ala Trp Lys Thr Val Leu Asp Ala Ala Leu Glu Gly
            130             135                 140
His Asp Asp Val Pro Thr Trp Tyr Val Asp Val Pro Thr Asn Ser Val
145                 150                 155                 160
Val Val Ala Val Lys Ala Gly Ala Gln Asp Val Ala Ala Gly Leu Val
                165                 170                 175
Glu Gly Ala Asp Val Pro Ser Asp Ala Val Thr Phe Val Glu Thr Asp
                180                 185                 190
Glu Thr Pro Arg Thr Met Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr
            195                 200                 205
Ile Gly Gly Arg Ser Arg Cys Ser Ile Gly Phe Ala Val Asn Gly Gly
    210                 215                 220
Phe Ile Thr Ala Gly His Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn
225                 230                 235                 240
Pro Thr Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala
                245                 250                 255
Phe Val Arg Thr Gly Ala Gly Val Asn Leu Leu Ala Gln Val Asn Asn
            260                 265                 270
Tyr Ser Gly Gly Arg Val Gln Val Ala Gly His Thr Ala Ala Pro Val
    275                 280                 285
Gly Ser Ala Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly
    290                 295                 300
Thr Ile Thr Ala Leu Asn Ser Ser Val Thr Tyr Pro Glu Gly Thr Val
305                 310                 315                 320
Arg Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
                325                 330                 335
Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val Thr Ser Gly Gly
            340                 345                 350
Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe Gln Pro Val Asn
            355                 360                 365
Pro Ile Leu Gln Ala Tyr Gly Leu Arg Met Ile Thr Thr Asp Ser Gly
    370                 375                 380
Ser Ser Pro Ala Pro Ala Pro Thr Ser Cys Thr Gly Tyr Ala Arg Thr
385                 390                 395                 400
Phe Thr Gly Thr Leu Ala Ala Gly Arg Ala Ala Ala Gln Pro Asn Gly
                405                 410                 415
Ser Tyr Val Gln Val Asn Arg Ser Gly Thr His Ser Val Cys Leu Asn
            420                 425                 430
Gly Pro Ser Gly Ala Asp Phe Asp Leu Tyr Val Gln Arg Trp Asn Gly
            435                 440                 445
Ser Ser Trp Val Thr Val Ala Gln Ser Thr Ser Pro Gly Ser Asn Glu
    450                 455                 460
Thr Ile Thr Tyr Arg Gly Asn Ala Gly Tyr Tyr Arg Tyr Val Val Asn
465                 470                 475                 480
Ala Ala Ser Gly Ser Gly Ala Tyr Thr Met Gly Leu Thr Leu Pro
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<210>   7
<211>   467
<212>   PRT
<213>   Cellulomonas strain 69B4
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<400> 7

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Asn Glu Pro Ala Pro Pro Gly Ser Ala Ser Ala Pro Pro Arg Leu Ala
1               5                   10                  15
Glu Lys Leu Asp Pro Asp Leu Leu Glu Ala Met Glu Arg Asp Leu Gly
            20                  25                  30
Leu Asp Ala Glu Glu Ala Ala Ala Thr Leu Ala Phe Gln His Asp Ala
            35                  40                  45
Ala Glu Thr Gly Glu Ala Leu Ala Glu Glu Leu Asp Glu Asp Phe Ala
        50                  55                  60
Gly Thr Trp Val Glu Asp Asp Val Leu Tyr Val Ala Thr Thr Asp Glu
65                  70                  75                  80
Asp Ala Val Glu Glu Val Glu Gly Glu Gly Ala Thr Ala Val Thr Val
            85                  90                  95
Glu His Ser Leu Ala Asp Leu Glu Ala Trp Lys Thr Val Leu Asp Ala
            100                 105                 110
Ala Leu Glu Gly His Asp Asp Val Pro Thr Trp Tyr Val Asp Val Pro
            115                 120                 125
Thr Asn Ser Val Val Val Ala Val Lys Ala Gly Ala Gln Asp Val Ala
            130                 135                 140
Ala Gly Leu Val Glu Gly Ala Asp Val Pro Ser Asp Ala Val Thr Phe
145                 150                 155                 160
Val Glu Thr Asp Glu Thr Pro Arg Thr Met Phe Asp Val Ile Gly Gly
                165                 170                 175
Asn Ala Tyr Thr Ile Gly Gly Arg Ser Arg Cys Ser Ile Gly Phe Ala
            180                 185                 190
Val Asn Gly Gly Phe Ile Thr Ala Gly His Cys Gly Arg Thr Gly Ala
            195                 200                 205
Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly
        210                 215                 220
Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala Gly Val Asn Leu Leu Ala
225                 230                 235                 240
Gln Val Asn Asn Tyr Ser Gly Gly Arg Val Gln Val Ala Gly His Thr
                245                 250                 255
Ala Ala Pro Val Gly Ser Ala Val Cys Arg Ser Gly Ser Thr Thr Gly
            260                 265                 270
Trp His Cys Gly Thr Ile Thr Ala Leu Asn Ser Ser Val Thr Tyr Pro
        275                 280                 285
Glu Gly Thr Val Arg Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro
    290                 295                 300
Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val
305                 310                 315                 320
Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe
                325                 330                 335
Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr Gly Leu Arg Met Ile Thr
            340                 345                 350
Thr Asp Ser Gly Ser Ser Pro Ala Pro Ala Pro Thr Ser Cys Thr Gly
            355                 360                 365
Tyr Ala Arg Thr Phe Thr Gly Thr Leu Ala Ala Gly Arg Ala Ala Ala
    370                 375                 380
Gln Pro Asn Gly Ser Tyr Val Gln Val Asn Arg Ser Gly Thr His Ser
385                 390                 395                 400
Val Cys Leu Asn Gly Pro Ser Gly Ala Asp Phe Asp Leu Tyr Val Gln
                405                 410                 415
Arg Trp Asn Gly Ser Ser Trp Val Thr Val Ala Gln Ser Thr Ser Pro
                420                 425                 430
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Gly Ser Asn Glu Thr Ile Thr Tyr Arg Gly Asn Ala Gly Tyr Tyr Arg
          435   440   445
Tyr Val Val Asn Ala Ala Ser Gly Ser Gly Ala Tyr Thr Met Gly Leu
          450   455   460
Thr Leu Pro
465

<210> 8
<211> 189
<212> PRT
<213> Cellulomonas spp.

<400> 8

Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr Ile Gly Gly Arg Ser Arg
1   5   10   15
Cys Ser Ile Gly Phe Ala Val Asn Gly Gly Phe Ile Thr Ala Gly His
              20   25   30
Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala
              35   40   45
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala
              50   55   60
Gly Val Asn Leu Leu Ala Gln Val Asn Asn Tyr Ser Gly Gly Arg Val
65   70   75   80
Gln Val Ala Gly His Thr Ala Ala Pro Val Gly Ser Ala Val Cys Arg
              85   90   95
Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Thr Ala Leu Asn
              100   105   110
Ser Ser Val Thr Tyr Pro Glu Gly Thr Val Arg Gly Leu Ile Arg Thr
              115   120   125
Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly
              130   135   140
Asn Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr
145   150   155   160
Gly Gly Thr Thr Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr
              165   170   175
Gly Leu Arg Met Ile Thr Thr Asp Ser Gly Ser Ser Pro
              180   185

<210> 9
<211> 28
<212> PRT
<213> Cellulomonas strain 69B4

<400> 9

Met Thr Pro Arg Thr Val Thr Arg Ala Leu Ala Val Ala Thr Ala Ala
1   5   10   15
Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala
              20   25

<210> 10
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<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<400> 10
acnacsggst ggcrgtgcgg cac   23

<210> 11
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<220>
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<222> (2)..(17)
<223> n is a, c, g, or t

<400> 11
angngccgcc ggagtcncc   19

<210> 12
<211> 58
<212> PRT
<213> Cellulomonas strain 69B4

<400> 12

Asp Gly Trp Asp Cys Gly Thr Ile Thr Ala Leu Asn Ser Ser Val Thr
1   5   10   15
Tyr Pro Glu Gly Thr Val Arg Gly Leu Ile Arg Thr Thr Val Cys Ala
            20   25   30
Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln
        35   40   45
Gly Val Thr Ser Gly Asp Ser Gly Gly Ser
    50   55

<210> 13
<211> 177
<212> DNA
<213> Cellulomonas strain 69B4

<400> 13
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gcaccgtccg cggcctgatc cgcaccaccg tctgcgccga gcccggcgac tccggtggct   120
cgctgctcgc cggcaaccag gcccagggcg tcacgtccgg cgactccggc ggctcat   177

<210> 14
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 14
cggggtaggt gaccgaggag ttgagcgcag tg   32

<210> 15
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 15
gctcgccggc aaccaggccc agggcgtcac gtc   33

<210> 16
<211> 34
<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<400> 16
aacggcgggt tcatcaccgc cggccactgc ggcc   34

<210> 17
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminus of the mature chain determined by MALDI-TOF analysis

<400> 17

Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr Ile Gly Gly Arg
1   5   10

<210> 18
<211> 189
<212> PRT
<213> Cellulomonas strain 69B4

<400> 18

Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr Ile Gly Gly Arg Ser Arg
1   5   10   15
Cys Ser Ile Gly Phe Ala Val Asn Gly Gly Phe Ile Thr Ala Gly His
            20   25   30
Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala
        35   40   45
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala

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        50                    55                     60
Gly Val Asn Leu Leu Ala Gln Val Asn Asn Tyr Ser Gly Gly Arg Val
65                    70                     75                     80
Gln Val Ala Gly His Thr Ala Ala Pro Val Gly Ser Ala Val Cys Arg
                85                    90                     95
Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Thr Ala Leu Asn
                100                   105                    110
Ser Ser Val Thr Tyr Pro Glu Gly Thr Val Arg Gly Leu Ile Arg Thr
                115                   120                    125
Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly
                130                   135                    140
Asn Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr
145                   150                    155                    160
Gly Gly Thr Thr Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr
                165                   170                    175
Gly Leu Arg Met Ile Thr Thr Asp Ser Gly Ser Ser Pro
                180                   185


<210>  19
<211>  184

<212>  PRT
<213>  Streptomyces griseus

<400>  19

Thr Pro Leu Ile Ala Gly Gly Glu Ala Ile Thr Thr Gly Gly Ser Arg
1                    5                     10                     15
Cys Ser Leu Gly Phe Asn Val Ser Val Asn Gly Val Ala His Ala Leu
                20                    25                     30
Thr Ala Gly His Cys Thr Asn Ile Ser Ala Ser Trp Ser Ile Gly Thr
                35                    40                     45
Arg Thr Gly Thr Ser Phe Pro Asn Asn Asp Tyr Gly Ile Ile Arg His
                50                    55                     60
Ser Asn Pro Ala Ala Ala Asp Gly Arg Val Tyr Leu Tyr Asn Gly Ser
65                    70                     75                     80
Tyr Gln Asp Ile Thr Thr Ala Gly Asn Ala Phe Val Gly Gln Ala Val
                85                    90                     95
Gln Arg Ser Gly Ser Thr Thr Gly Leu Arg Ser Gly Ser Val Thr Gly
                100                   105                    110
Leu Asn Ala Thr Val Asn Tyr Gly Ser Ser Gly Ile Val Tyr Gly Met
                115                   120                    125
Ile Gln Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu
                130                   135                    140
Phe Ala Gly Ser Thr Ala Leu Gly Leu Thr Ser Gly Gly Ser Gly Asn
145                   150                    155                    160
Cys Arg Thr Gly Gly Thr Thr Phe Tyr Gln Pro Val Thr Glu Ala Leu
                165                   170                    175
Ser Ala Tyr Gly Ala Thr Val Leu
                180


<210>  20
<211>  174
<212>  PRT
<213>  Streptomyces fradiae

<400>  20
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1               5                   10                  15
Leu Gly Phe Asn Val Arg Ser Ser Ser Gly Ala Thr Tyr Ala Leu Thr
            20                  25                  30
Ala Gly His Cys Thr Glu Ile Ala Ser Thr Trp Tyr Thr Asn Ser Gly
            35                  40                  45
Gln Thr Ser Leu Leu Gly Thr Arg Ala Gly Thr Ser Phe Pro Gly Asn
    50                  55                  60
Asp Tyr Gly Leu Ile Arg His Ser Asn Ala Ser Ala Ala Asp Gly Arg
65                  70                  75                  80
Val Tyr Leu Tyr Asn Gly Ser Tyr Arg Asp Ile Thr Gly Ala Gly Asn
            85                  90                  95
Ala Tyr Val Gly Gln Thr Val Gln Arg Ser Gly Ser Thr Thr Gly Leu
            100                 105                 110
His Ser Gly Arg Val Thr Gly Leu Asn Ala Thr Val Asn Tyr Gly Gly
    115                 120                 125
Gly Asp Ile Val Ser Gly Leu Ile Gln Thr Asn Val Cys Ala Glu Pro
    130                 135                 140
Gly Asp Ser Gly Gly Ala Leu Phe Ala Gly Ser Thr Ala Leu Gly Leu
145                 150                 155                 160
Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr
            165                 170
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<210> 21
<211> 188
<212> PRT
<213> Streptomyces lividans

<400> 21

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Asn Lys Leu Ile Gln Gly Gly Asp Ala Ile Tyr Ala Ser Ser Trp Arg
1               5                   10                  15
Cys Ser Leu Gly Phe Asn Val Arg Thr Ser Ser Gly Ala Glu Tyr Phe
            20                  25                  30
Leu Thr Ala Gly His Cys Thr Asp Gly Ala Gly Ala Trp Arg Ala Ser
            35                  40                  45
Ser Gly Gly Thr Val Ile Gly Gln Thr Ala Gly Ser Ser Phe Pro Gly
    50                  55                  60
Asn Asp Tyr Gly Ile Val Gln Tyr Thr Gly Ser Val Ser Arg Pro Gly
65                  70                  75                  80
Thr Ala Asn Gly Val Asp Ile Thr Arg Ala Ala Thr Pro Ser Val Gly
            85                  90                  95
Thr Thr Val Ile Arg Asp Gly Ser Thr Thr Gly Thr His Ser Gly Arg
            100                 105                 110
Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Gly Asp Val Val
            115                 120                 125
Gly Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
    130                 135                 140
Gly Ser Leu Tyr Gly Ser Asn Gly Thr Ala Tyr Gly Leu Thr Ser Gly
145                 150   .               155                 160
Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val
            165                 170                 175
Thr Glu Ala Leu Ser Ala Tyr Gly Val Ser Val Tyr
            180                 185
```

<210> 22
<211> 188

<212> PRT
<213> Streptomyces coelicolor

<400> 22

Asn Lys Leu Ile Gln Gly Gly Asp Ala Ile Tyr Ala Ser Ser Trp Arg
1   5   10   15
Cys Ser Leu Gly Phe Asn Val Arg Thr Ser Ser Gly Ala Glu Tyr Phe
            20   25   30
Leu Thr Ala Gly His Cys Thr Asp Gly Ala Gly Ala Trp Arg Ala Ser
            35   40   45
Ser Gly Gly Thr Val Ile Gly Gln Thr Ala Gly Ser Ser Phe Pro Gly
            50   55   60
Asn Asp Tyr Gly Ile Val Gln Tyr Thr Gly Ser Val Ser Arg Pro Gly
65   70   75   80
Thr Ala Asn Gly Val Asp Ile Thr Arg Ala Ala Thr Pro Ser Val Gly
                85   90   95
Thr Thr Val Ile Arg Asp Gly Ser Thr Thr Gly Thr His Ser Gly Arg
            100   105   110
Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Gly Asp Val Val
            115   120   125
Gly Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
            130   135   140
Gly Ser Leu Tyr Gly Ser Asn Gly Thr Ala Tyr Gly Leu Thr Ser Gly
145   150   155   160
Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val
                165   170   175
Thr Glu Ala Leu Ser Ala Tyr Gly Val Ser Val Tyr
                180   185

<210> 23
<211> 189
<212> PRT

<213> Streptomyces albogriseolus

<400> 23

Thr Lys Leu Ile Gln Gly Gly Asp Ala Ile Tyr Ala Ser Ser Trp Arg
1   5   10   15
Cys Ser Leu Gly Phe Asn Val Arg Ser Ser Ser Gly Val Asp Tyr Phe
            20   25   30
Leu Thr Ala Gly His Cys Thr Asp Gly Ala Gly Thr Trp Tyr Ser Asn
            35   40   45
Ser Ala Arg Thr Thr Ala Ile Gly Ser Thr Ala Gly Ser Ser Phe Pro
            50   55   60
Gly Asn Asp Tyr Gly Ile Val Arg Tyr Thr Gly Ser Val Ser Arg Pro
65   70   75   80
Gly Thr Ala Asn Gly Val Asp Ile Thr Arg Ala Ala Thr Pro Ser Val
                85   90   95
Gly Thr Thr Val Ile Arg Asp Gly Ser Thr Thr Gly Thr His Ser Gly
            100   105   110
Arg Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Gly Asp Ile
            115   120   125
Val Ser Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro Gly Asp Ser
            130   135   140
Gly Gly Pro Leu Tyr Gly Ser Asn Gly Thr Ala Tyr Gly Leu Thr Ser

```
            145                  150                  155                  160
Gly Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro
                165                  170                  175
Val Thr Glu Ala Leu Ser Ala Tyr Gly Val Ser Val Tyr
            180                  185


<210>  24
<211>  188
<212>  PRT
<213>  Streptomyces griseus


<400>  24


Thr Lys Leu Ile Ser Gly Gly Asp Ala Ile Tyr Ser Ser Thr Gly Arg
1                   5                   10                  15
Cys Ser Leu Gly Phe Asn Val Arg Ser Gly Ser Thr Tyr Tyr Phe Leu
                20                  25                  30
Thr Ala Gly His Cys Thr Asp Gly Ala Thr Thr Trp Trp Ala Asn Ser
            35                  40                  45
Ala Arg Thr Thr Val Leu Gly Thr Thr Ser Gly Ser Ser Phe Pro Asn
            50                  55                  60
Asn Asp Tyr Gly Ile Val Arg Tyr Thr Asn Thr Thr Ile Pro Lys Asp
65                  70                  75                  80
Gly Thr Val Gly Gly Gln Asp Ile Thr Ser Ala Ala Asn Ala Thr Val
                85                  90                  95
Gly Met Ala Val Thr Arg Arg Gly Ser Thr Thr Gly Thr His Ser Gly
            100                 105                 110
Ser Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Gly Asp Val
            115                 120                 125
Val Tyr Gly Met Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser
            130                 135                 140
Gly Gly Pro Leu Tyr Ser Gly Thr Arg Ala Ile Gly Leu Thr Ser Gly
145                 150                 155                 160
Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val
                165                 170                 175
Thr Glu Ala Leu Ser Ala Tyr Gly Val Ser Val Tyr
            180                 185


<210>  25
<211>  188
<212>  PRT
<213>  Streptomyces griseus


<400>  25


Val Leu Gly Gly Gly Ala Ile Tyr Gly Gly Gly Ser Arg Cys Ser Ala
1                   5                   10                  15
Ala Phe Asn Val Thr Lys Gly Gly Ala Arg Tyr Phe Val Thr Ala Gly
                20                  25                  30
His Cys Thr Asn Ile Ser Ala Asn Trp Ser Ala Ser Ser Gly Gly Ser
            35                  40                  45
Val Val Gly Val Arg Glu Gly Thr Ser Phe Pro Thr Asn Asp Tyr Gly
            50                  55                  60
Ile Val Arg Tyr Thr Asp Gly Ser Ser Pro Ala Gly Thr Val Asp Leu
65                  70                  75                  80
Tyr Asn Gly Ser Thr Gln Asp Ile Ser Ser Ala Ala Asn Ala Val Val
                85                  90                  95
```

```
Gly Gln Ala Ile Lys Lys Ser Gly Ser Thr Thr Lys Val Thr Ser Gly
            100                 105                 110
Thr Val Thr Ala Val Asn Val Thr Val Asn Tyr Gly Asp Gly Pro Val
            115                 120                 125
Tyr Asn Met Gly Arg Thr Thr Ala Cys Ser Ala Gly Gly Asp Ser Gly
        130                 135                 140
Gly Ala His Phe Ala Gly Ser Val Ala Leu Gly Ile His Ser Gly Ser
145                 150                 155                 160
Ser Gly Cys Ser Gly Thr Ala Gly Ser Ala Ile His Gln Pro Val Thr
                165                 170                 175
Lys Ala Leu Ser Ala Tyr Gly Val Thr Val Tyr Leu
            180                 185
```

<210> 26
<211> 190
<212> PRT
<213> Streptomyces fradiae

<400> 26

```
Gln Arg Glu Val Ala Gly Gly Asp Ala Ile Tyr Gly Gly Gly Ser Arg
1               5                   10                  15
Cys Ser Ala Ala Phe Asn Val Thr Lys Asn Gly Val Arg Tyr Phe Leu
            20                  25                  30
Thr Ala Gly His Cys Thr Asn Leu Ser Ser Thr Trp Ser Ser Thr Ser
        35                  40                  45
Gly Gly Thr Ser Ile Gly Val Arg Glu Gly Thr Ser Phe Pro Thr Asn
    50                  55                  60
Asp Tyr Gly Ile Val Arg Tyr Thr Thr Thr Thr Asn Val Asp Gly Arg
65                  70                  75                  80
Val Asn Leu Tyr Asn Gly Gly Tyr Gln Asp Ile Ala Ser Ala Ala Asp
                85                  90                  95
Ala Val Val Gly Gln Ala Ile Lys Lys Ser Gly Ser Thr Thr Lys Val
            100                 105                 110
Thr Ser Gly Thr Val Ser Ala Val Asn Val Thr Val Asn Tyr Ser Asp
            115                 120                 125
Gly Pro Val Tyr Gly Met Val Arg Thr Thr Ala Cys Ser Ala Gly Gly
        130                 135                 140
Asp Ser Gly Gly Ala His Phe Ala Gly Ser Val Ala Leu Gly Ile His
145                 150                 155                 160
Ser Gly Ser Ser Gly Cys Thr Gly Thr Asn Gly Ser Ala Ile His Gln
                165                 170                 175
Pro Val Arg Glu Ala Leu Ser Ala Tyr Gly Val Asn Val Tyr
            180                 185                 190
```

<210> 27
<211> 190
<212> PRT
<213> Streptomyces albogriseolus

<400> 27

```
Lys Pro Phe Ile Ala Gly Gly Asp Ala Ile Thr Gly Asn Gly Gly Arg
1               5                   10                  15
Cys Ser Leu Gly Phe Asn Val Thr Lys Gly Gly Glu Pro His Phe Leu
            20                  25                  30
Thr Ala Gly His Cys Thr Glu Gly Ile Ser Thr Trp Ser Asp Ser Ser
```

```
                35                    40                    45
Gly Gln Val Ile Gly Glu Asn Ala Ala Ser Ser Phe Pro Gly Asp Asp
    50                    55                    60
Tyr Gly Leu Val Lys Tyr Thr Ala Asp Val Ala His Pro Ser Gln Val
65                    70                    75                    80
Asn Leu Tyr Asp Gly Ser Ser Gln Ser Ile Ser Gly Ala Ala Glu Ala
                85                    90                    95
Ala Val Gly Met Gln Val Thr Arg Ser Gly Ser Thr Thr Gln Val His
            100                   105                   110
Ser Gly Thr Val Thr Gly Leu Asp Ala Thr Val Asn Tyr Gly Asn Gly
            115                   120                   125
Asp Ile Val Asn Gly Leu Ile Gln Thr Asp Val Cys Ala Glu Pro Gly
    130                   135                   140
Asp Ser Gly Gly Ser Leu Phe Ser Gly Asp Lys Ala Val Gly Leu Thr
145                   150                   155                   160
Ser Gly Gly Ser Gly Asp Cys Thr Ser Gly Gly· Thr Thr Phe Phe Gln
            165                   170                   175
Pro Val Thr Glu Ala Leu Ser Ala Thr Gly Thr Gln Ile Gly
            180                   185                   190


<210>   28
<211>   190
<212>   PRT
<213>   Streptomyces coelicolor


<400>   28

Lys Pro Phe Val Ala Gly Gly Asp Ala Ile Thr Gly Gly Gly Gly Arg
1                     5                     10                    15
Cys Ser Leu Gly Phe Asn Val Thr Lys Gly Gly Glu Pro Tyr Phe Ile
            20                    25                    30
Thr Ala Gly His Cys Thr Glu Ser Ile Ser Thr Trp Ser Asp Ser Ser
            35                    40                    45
Gly Asn Val Ile Gly Glu Asn Ala Ala Ser Ser Phe Pro Asp Asn Asp
    50                    55                    60
Tyr Gly Leu Val Lys Tyr Thr Ala Asp Val Asp His Pro Ser Glu Val
65                    70                    75                    80
Asn Leu Tyr Asn Gly Ser Ser Gln Ala Ile Ser Gly Ala Ala Glu Ala
                85                    90                    95
Thr Val Gly Met Gln Val Thr Arg Ser Gly Ser Thr Thr Gln Val His
            100                   105                   110
Asp Gly Thr Val Thr Gly Leu Asp Ala Thr Val Asn Tyr Gly Asn Gly
            115                   120                   125
Asp Ile Val Asn Gly Leu Ile Gln Thr Asp Val Cys Ala Glu Pro Gly
    130                   135                   140
Asp Ser Gly Gly Ser Leu Phe Ser Gly Asp Gln Ala Ile Gly Leu Thr
145                   150                   155                   160
Ser Gly Gly Ser Gly Asp Cys Thr Ser Gly Gly Glu Thr Phe Phe Gln
            165                   170                   175
Pro Val Thr Glu Ala Leu Ser Ala Thr Gly Thr Gln Ile Gly
            180                   185                   190


<210>   29
<211>   191
<212>   PRT
<213>   Streptomyces griseus
```

<400> 29

```
Thr Pro Leu Ile Ala Gly Gly Asp Ala Ile Trp Gly Ser Gly Ser Arg
1               5                   10                  15
Cys Ser Leu Gly Phe Asn Val Val Lys Gly Gly Glu Pro Tyr Phe Leu
            20                  25                  30
Thr Ala Gly His Cys Thr Glu Ser Val Thr Ser Trp Ser Asp Thr Gln
            35                  40                  45
Gly Gly Ser Glu Ile Gly Ala Asn Glu Gly Ser Ser Phe Pro Glu Asn
    50                  55                  60
Asp Tyr Gly Leu Val Lys Tyr Thr Ser Asp Thr Ala His Pro Ser Glu
65                  70                  75                  80
Val Asn Leu Tyr Asp Gly Ser Thr Gln Ala Ile Thr Gln Ala Gly Asp
            85                  90                  95
Ala Thr Val Gly Gln Ala Val Thr Arg Ser Gly Ser Thr Thr Gln Val
            100                 105                 110
His Asp Gly Glu Val Thr Ala Leu Asp Ala Thr Val Asn Tyr Gly Asn
            115                 120                 125
Gly Asp Ile Val Asn Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro
    130                 135                 140
Gly Asp Ser Gly Gly Ala Leu Phe Ala Gly Asp Thr Ala Leu Gly Leu
145                 150                 155                 160
Thr Ser Gly Gly Ser Gly Asp Cys Ser Ser Gly Gly Thr Thr Phe Phe
            165                 170                 175
Gln Pro Val Pro Glu Ala Leu Ala Ala Tyr Gly Ala Glu Ile Gly
            180                 185                 190
```

<210>   30
<211>   200
<212>   PRT
<213>   Streptomyces lividans

<400>   30

```
Lys Thr Phe Ala Ser Gly Gly Asp Ala Ile Phe Gly Gly Gly Ala Arg
1               5                   10                  15
Cys Ser Leu Gly Phe Asn Val Thr Ala Gly Asp Gly Ser Ala Ala Phe
            20                  25                  30
Leu Thr Arg Gly His Cys Gly Gly Gly Ala Thr Met Trp Ser Asp Ala
            35                  40                  45
Gln Gly Gly Gln Pro Ile Ala Thr Val Asp Gln Ala Val Phe Pro Pro
    50                  55                  60
Glu Gly Asp Phe Gly Leu Val Arg Tyr Asp Gly Pro Ser Thr Glu Ala
65                  70                  75                  80
Pro Ser Glu Val Asp Leu Gly Asp Gln Thr Leu Pro Ile Ser Gly Ala
            85                  90                  95
Ala Glu Ala Ser Val Gly Gln Glu Val Phe Arg Met Gly Ser Thr Thr
            100                 105                 110
Gly Leu Ala Asp Gly Gln Val Leu Gly Leu Asp Val Thr Val Asn Tyr
            115                 120                 125
Pro Glu Gly Thr Val Thr Gly Leu Ile Gln Thr Asp Val Cys Ala Glu
    130                 135                 140
Pro Gly Asp Ser Gly Gly Ser Leu Phe Thr Arg Asp Gly Leu Ala Ile
145                 150                 155                 160
Arg Leu Thr Ser Gly Gly Thr Arg Asp Cys Thr Ser Gly Gly Glu Thr
            165                 170                 175
Phe Phe Gln Pro Val Thr Thr Ala Leu Ala Ala Val Gly Gly Thr Leu
```

```
            180                 185                        190
Gly Gly Glu Asp Gly Gly Asp Gly
        195                     200


<210>  31
<211>  201
<212>  PRT
<213>  Streptomyces coelicolor


<400>  31

Lys Thr Phe Ala Ser Gly Gly Asp Ala Ile Phe Gly Gly Gly Ala Arg
1               5                   10                  15
Cys Ser Leu Gly Phe Asn Val Thr Ala Gly Asp Gly Ser Pro Ala Phe
            20                  25                  30
Leu Thr Ala Gly His Cys Gly Val Ala Ala Asp Gln Trp Ser Asp Ala
        35                  40                  45
Gln Gly Gly Gln Pro Ile Ala Thr Val Asp Gln Ala Val Phe Pro Gly
    50                  55                  60
Glu Gly Asp Phe Ala Leu Val Arg Tyr Asp Asp Pro Ala Thr Glu Ala
65                  70                  75                  80
Pro Ser Glu Val Asp Leu Gly Asp Gln Thr Leu Pro Ile Ser Gly Ala
                85                  90                  95
Ala Glu Ala Ala Val Gly Gln Glu Val Phe Arg Met Gly Ser Thr Thr
            100                 105                 110
Gly Leu Ala Asp Gly Gln Val Leu Gly Leu Asp Ala Thr Val Asn Tyr
        115                 120                 125
Pro Glu Gly Met Val Thr Gly Leu Ile Gln Thr Asp Val Cys Ala Glu
    130                 135                 140
Pro Gly Asp Ser Gly Gly Ser Leu Phe Thr Arg Asp Gly Leu Ala Ile
145                 150                 155                 160
Gly Leu Thr Ser Gly Gly Ser Gly Asp Cys Thr Val Gly Gly Glu Thr
                165                 170                 175
Phe Phe Gln Pro Val Thr Thr Ala Leu Ala Ala Val Gly Ala Thr Leu
            180                 185                 190
Gly Gly Glu Asp Gly Gly Ala Gly Ala
        195                 200


<210>  32
<211>  68
<212>  PRT
<213>  Streptomyces platensis


<400>  32

Val Asp Gly Leu Ile Gln Thr Asp Val Cys Ala Glu Pro Gly Asp Ser
1               5                   10                  15
Gly Gly Ala Leu Phe Asp Gly Asp Ala Ala Ile Gly Leu Thr Ser Gly
            20                  25                  30
Gly Ser Gly Asp Cys Ser Gln Gly Gly Glu Thr Phe Phe Gln Pro Val
        35                  40                  45
Thr Glu Ala Leu Lys Ala Tyr Gly Ala Gln Ile Gly Gly Gly Gln Gly
    50                  55                  60
Glu Pro Pro Glu
65


<210>  33
```

<211> 201
<212> PRT
<213> Streptomyces coelicolor

<400> 33

```
Thr Thr Arg Leu Asn Gly Ala Glu Pro Ile Leu Ser Thr Ala Gly Arg
1               5                   10                  15
Cys Ser Ala Gly Phe Asn Val Thr Asp Gly Thr Ser Asp Phe Ile Leu
            20                  25                  30
Thr Ala Gly His Cys Gly Pro Thr Gly Ser Val Trp Phe Gly Asp Arg
        35                  40                  45
Pro Gly Asp Gly Gln Val Gly Arg Thr Val Ala Gly Ser Phe Pro Gly
    50                  55                  60
Asp Asp Phe Ser Leu Val Glu Tyr Ala Asn Gly Lys Ala Gly Asp Gly
65                  70                  75                  80
Ala Asp Val Val Ala Val Gly Asp Gly Lys Gly Val Arg Ile Thr Gly
            85                  90                  95
Ala Gly Glu Pro Ala Val Gly Gln Arg Val Phe Arg Ser Gly Ser Thr
            100                 105                 110
Ser Gly Leu Arg Asp Gly Arg Val Thr Ala Leu Asp Ala Thr Val Asn
        115                 120                 125
Tyr Pro Glu Gly Thr Val Thr Gly Leu Ile Glu Thr Asp Val Cys Ala
    130                 135                 140
Glu Pro Gly Asp Ser Gly Gly Pro Met Phe Ser Glu Gly Val Ala Leu
145                 150                 155                 160
Gly Val Thr Ser Gly Gly Ser Gly Asp Cys Ala Lys Gly Gly Thr Thr
            165                 170                 175
Phe Phe Gln Pro Leu Pro Glu Ala Met Ala Ser Leu Gly Val Arg Leu
            180                 185                 190
Ile Val Pro Gly Arg Glu Gly Ala Ala
            195                 200
```

<210> 34
<211> 188
<212> PRT
<213> Metarhizium anisopliae

<400> 34

```
Ala Thr Val Gln Gly Gly Asp Val Tyr Tyr Ile Asn Arg Ser Ser Arg
1               5                   10                  15
Cys Ser Ile Gly Phe Ala Val Thr Thr Gly Phe Val Ser Ala Gly His
            20                  25                  30
Cys Gly Gly Ser Gly Ala Ser Ala Thr Thr Ser Ser Gly Glu Ala Leu
        35                  40                  45
Gly Thr Phe Ser Gly Ser Val Phe Pro Gly Ser Ala Asp Met Ala Tyr
    50                  55                  60
Val Arg Thr Val Ser Gly Thr Val Leu Arg Gly Tyr Ile Asn Gly Tyr
65                  70                  75                  80
Gly Gln Gly Ser Phe Pro Val Ser Gly Ser Ser Glu Ala Ala Val Gly
            85                  90                  95
Ala Ser Ile Cys Arg Ser Gly Ser Thr Thr Gln Val His Cys Gly Thr
            100                 105                 110
Ile Gly Ala Lys Gly Ala Thr Val Asn Tyr Pro Gln Gly Ala Val Ser
        115                 120                 125
Gly Leu Thr Arg Thr Ser Val Cys Ala Glu Pro Gly Asp Ser Gly Gly
```

```
                    130                   135                   140
Ser Phe Tyr Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Ser
145                   150                   155                   160
Gly Asp Cys Ser Arg Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Arg
                165                   170                   175
Ile Leu Gln Thr Tyr Gly Leu Thr Leu Val Thr Ala
            180                   185


<210>  35
<211>  195
<212>  PRT
<213>  Streptomyces griseus


<400>  35

Ala Asp Ile Arg Gly Gly Asp Ala Tyr Tyr Met Asn Gly Ser Gly Arg
1                   5                   10                   15
Cys Ser Val Gly Phe Ser Val Thr Arg Gly Thr Gln Asn Gly Phe Ala
                20                   25                   30
Thr Ala Gly His Cys Gly Arg Val Gly Thr Thr Thr Asn Gly Val Asn
            35                   40                   45
Gln Gln Ala Gln Gly Thr Phe Gln Gly Ser Thr Phe Pro Gly Arg Asp
        50                   55                   60
Ile Ala Trp Val Ala Thr Asn Ala Asn Trp Thr Pro Arg Pro Leu Val
65                   70                   75                   80
Asn Gly Tyr Gly Arg Gly Asp Val Thr Val Ala Gly Ser Thr Ala Ser
                85                   90                   95
Val Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His
            100                   105                   110
Cys Gly Thr Ile Gln Gln Leu Asn Thr Ser Val Thr Tyr Pro Glu Gly
        115                   120                   125
Thr Ile Ser Gly Val Thr Arg Thr Ser Val Cys Ala Glu Pro Gly Asp
        130                   135                   140
Ser Gly Gly Ser Tyr Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser
145                   150                   155                   160
Gly Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Tyr Phe Gln Pro
                165                   170                   175
Ile Asn Pro Leu Leu Gln Ala Tyr Gly Leu Thr Leu Val Thr Ser Gly
            180                   185                   190
Gly Gly Thr
        195


<210>  36
<211>  197
<212>  PRT
<213>  Streptomyces coelicolor


<400>  36

Tyr Asp Leu Arg Gly Gly Glu Ala Tyr Tyr Ile Asn Asn Ser Ser Arg
1                   5                   10                   15
Cys Ser Ile Gly Phe Pro Ile Thr Lys Gly Thr Gln Gln Gly Phe Ala
                20                   25                   30
Thr Ala Gly His Cys Gly Arg Ala Gly Ser Ser Thr Thr Gly Ala Asn
            35                   40                   45
Arg Val Ala Gln Gly Thr Phe Gln Gly Ser Ile Phe Pro Gly Arg Asp
        50                   55                   60
```

```
Met Ala Trp Val Ala Thr Asn Ser Ser Trp Thr Ala Thr Pro Tyr Val
65                  70                  75                  80
Leu Gly Ala Gly Gly Gln Asn Val Gln Val Thr Gly Ser Thr Ala Ser
                85                  90                  95
Pro Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His
            100                 105                 110
Cys Gly Thr Val Thr Gln Leu Asn Thr Ser Val Thr Tyr Gln Glu Gly
            115                 120                 125
Thr Ile Ser Pro Val Thr Arg Thr Thr Val Cys Ala Glu Pro Gly Asp
        130                 135                 140
Ser Gly Gly Ser Phe Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser
145                 150                 155                 160
Gly Gly Ser Gly Asp Cys Arg Thr Gly Gly Glu Thr Phe Phe Gln Pro
                165                 170                 175
Ile Asn Ala Leu Leu Gln Asn Tyr Gly Leu Thr Leu Lys Thr Thr Gly
                180                 185                 190
Gly Asp Asp Gly Gly
        195


<210>    37
<211>    189
<212>    PRT
<213>    Streptomyces spp.


<400>    37

Tyr Asp Leu Val Gly Gly Asp Ala Tyr Tyr Ile Gly Asn Gly Arg Cys
1                   5                   10                  15
Ser Ile Gly Phe Ser Val Arg Gln Gly Ser Thr Pro Gly Phe Val Thr
                20                  25                  30
Ala Gly His Cys Gly Ser Val Gly Asn Ala Thr Thr Gly Phe Asn Arg
            35                  40                  45
Val Ser Gln Gly Thr Phe Arg Gly Ser Trp Phe Pro Gly Arg Asp Met
        50                  55                  60
Ala Trp Val Ala Val Asn Ser Asn Trp Thr Pro Thr Ser Leu Val Arg
65                  70                  75                  80
Asn Ser Gly Ser Gly Val Arg Val Thr Gly Ser Thr Gln Ala Thr Val
                85                  90                  95
Gly Ser Ser Ile Cys Arg Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly
            100                 105                 110
Thr Ile Gln Gln His Asn Thr Ser Val Thr Tyr Pro Gln Gly Thr Ile
        115                 120                 125
Thr Gly Val Thr Arg Thr Ser Ala Cys Ala Gln Pro Gly Asp Ser Gly
        130                 135                 140
Gly Ser Phe Ile Ser Gly Thr Gln Ala Gln Gly Val Thr Ser Gly Gly
145                 150                 155                 160
Ser Gly Asn Cys Ser Ile Gly Gly Thr Thr Phe His Gln Pro Val Asn
                165                 170                 175
Pro Ile Leu Ser Gln Tyr Gly Leu Thr Leu Val Arg Ser
                180                 185


<210>    38
<211>    187
<212>    PRT
<213>    Streptomyces spp.


<400>    38
```

```
Tyr Asp Leu Val Gly Gly Asp Ala Tyr Tyr Met Gly Gly Gly Arg Cys
1               5                   10                  15
Ser Val Gly Phe Ser Val Thr Gln Gly Ser Thr Pro Gly Phe Ala Thr
            20                  25                  30
Ala Gly His Cys Gly Thr Val Gly Thr Ser Thr Thr Gly Tyr Asn Gln
        35                  40                  45
Ala Ala Gln Gly Thr Phe Glu Glu Ser Ser Phe Pro Gly Asp Asp Met
    50                  55                  60
Ala Trp Val Ser Val Asn Ser Asp Trp Asn Thr Thr Pro Thr Val Asn
65                  70                  75                  80
Glu Gly Glu Val Thr Val Ser Gly Ser Thr Glu Ala Ala Val Gly Ala
                85                  90                  95
Ser Ile Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile
            100                 105                 110
Gln Gln His Asn Thr Ser Val Thr Tyr Pro Glu Gly Thr Ile Thr Gly
        115                 120                 125
Val Thr Arg Thr Ser Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser
    130                 135                 140
Tyr Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly
145                 150                 155                 160
Asn Cys Thr Ser Gly Gly Thr Thr Tyr His Gln Pro Ile Asn Pro Leu
            165                 170                 175
Leu Ser Ala Tyr Gly Leu Asp Leu Val Thr Gly
        180                 185
```

<210> 39
<211> 193
<212> PRT
<213> Streptomyces coelicolor

<400> 39

```
Glu Asp Leu Val Gly Gly Asp Ala Tyr Tyr Ile Asp Asp Gln Ala Arg
1               5                   10                  15
Cys Ser Ile Gly Phe Ser Val Thr Lys Asp Asp Gln Glu Gly Phe Ala
            20                  25                  30
Thr Ala Gly His Cys Gly Asp Pro Gly Ala Thr Thr Thr Gly Tyr Asn
        35                  40                  45
Glu Ala Asp Gln Gly Thr Phe Gln Ala Ser Thr Phe Pro Gly Lys Asp
    50                  55                  60
Met Ala Trp Val Gly Val Asn Ser Asp Trp Thr Ala Thr Pro Asp Val
65                  70                  75                  80
Lys Ala Glu Gly Gly Glu Lys Ile Gln Leu Ala Gly Ser Val Glu Ala
                85                  90                  95
Leu Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His
            100                 105                 110
Cys Gly Thr Ile Gln Gln His Asp Thr Ser Val Thr Tyr Pro Glu Gly
        115                 120                 125
Thr Val Asp Gly Leu Thr Glu Thr Thr Val Cys Ala Glu Pro Gly Asp
    130                 135                 140
Ser Gly Gly Pro Phe Val Ser Gly Val Gln Ala Gln Gly Thr Thr Ser
145                 150                 155                 160
Gly Gly Ser Gly Asp Cys Thr Asn Gly Gly Thr Thr Phe Tyr Gln Pro
            165                 170                 175
Val Asn Pro Leu Leu Ser Asp Phe Gly Leu Thr Leu Lys Thr Thr Ser
        180                 185                 190
```

Ala

<210>   40
<211>   187
<212>   PRT
<213>   Thermobifida fusca

<400>   40

Leu Ala Ala Ile Ile Gly Gly Asn Pro Tyr Tyr Phe Gly Asn Tyr Arg
1   5   10   15
Cys Ser Ile Gly Phe Ser Val Arg Gln Gly Ser Gln Thr Gly Phe Ala
            20   25   30
Thr Ala Gly His Cys Gly Ser Thr Gly Thr Arg Val Ser Ser Pro Ser
        35   40   45
Gly Thr Val Ala Gly Ser Tyr Phe Pro Gly Arg Asp Met Gly Trp Val
    50   55   60
Arg Ile Thr Ser Ala Asp Thr Val Thr Pro Leu Val Asn Arg Tyr Asn
65   70   75   80
Gly Gly Thr Val Thr Val Thr Gly Ser Gln Glu Ala Ala Thr Gly Ser
                85   90   95
Ser Val Cys Arg Ser Gly Ala Thr Thr Gly Trp Arg Cys Gly Thr Ile
            100   105   110
Gln Ser Lys Asn Gln Thr Val Arg Tyr Ala Glu Gly Thr Val Thr Gly
        115   120   125
Leu Thr Arg Thr Thr Ala Cys Ala Glu Gly Gly Asp Ser Gly Gly Pro
    130   135   140
Trp Leu Thr Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Thr Gly
145   150   155   160
Asp Cys Arg Ser Gly Gly Ile Thr Phe Phe Gln Pro Ile Asn Pro Leu
            165   170   175
Leu Ser Tyr Phe Gly Leu Gln Leu Val Thr Gly
            180   185

<210>   41
<211>   198
<212>   PRT
<213>   Lysobacter enzymogenes

<400>   41

Ala Asn Ile Val Gly Gly Ile Glu Tyr Ser Ile Asn Asn Ala Ser Leu
1   5   10   15
Cys Ser Val Gly Phe Ser Val Thr Arg Gly Ala Thr Lys Gly Phe Val
            20   25   30
Thr Ala Gly His Cys Gly Thr Val Asn Ala Thr Ala Arg Ile Gly Gly
        35   40   45
Ala Val Val Gly Thr Phe Ala Ala Arg Val Phe Pro Gly Asn Asp Arg
    50   55   60
Ala Trp Val Ser Leu Thr Ser Ala Gln Thr Leu Leu Pro Arg Val Ala
65   70   75   80
Asn Gly Ser Ser Phe Val Thr Val Arg Gly Ser Thr Glu Ala Ala Val
                85   90   95
Gly Ala Ala Val Cys Arg Ser Gly Arg Thr Thr Gly Tyr Gln Cys Gly
            100   105   110
Thr Ile Thr Ala Lys Asn Val Thr Ala Asn Tyr Ala Glu Gly Ala Val

```
        115                    120                    125
Arg Gly Leu Thr Gln Gly Asn Ala Cys Met Gly Arg Gly Asp Ser Gly
    130                    135                    140
Gly Ser Trp Ile Thr Ser Ala Gly Gln Ala Gln Gly Val Met Ser Gly
145                    150                    155                    160
Gly Asn Val Gln Ser Asn Gly Asn Asn Cys Gly Ile Pro Ala Ser Gln
                   165                    170                    175
Arg Ser Ser Leu Phe Glu Arg Leu Gln Pro Ile Leu Ser Gln Tyr Gly
                   180                    185                    190
Leu Ser Leu Val Thr Gly
                   195


<210>   42
<211>   189
<212>   PRT
<213>   Streptomyces coelicolor


<400>   42

Ala Ala Gly Thr Val Gly Gly Asp Pro Tyr Tyr Thr Gly Asn Val Arg
1                   5                    10                    15
Cys Ser Ile Gly Phe Ser Val His Gly Gly Phe Val Thr Ala Gly His
                   20                    25                    30
Cys Gly Arg Ala Gly Ala Gly Val Ser Gly Trp Asp Arg Ser Tyr Ile
               35                    40                    45
Gly Thr Phe Gln Gly Ser Ser Phe Pro Asp Asn Asp Tyr Ala Trp Val
           50                    55                    60
Ser Val Gly Ser Gly Trp Trp Thr Val Pro Val Val Leu Gly Trp Gly
65                    70                    75                    80
Thr Val Ser Asp Gln Leu Val Arg Gly Ser Asn Val Ala Pro Val Gly
                   85                    90                    95
Ala Ser Ile Cys Arg Ser Gly Ser Thr Thr His Trp His Cys Gly Thr
               100                    105                    110
Val Leu Ala His Asn Glu Thr Val Asn Tyr Ser Asp Gly Ser Val Val
               115                    120                    125
His Gln Leu Thr Lys Thr Ser Val Cys Ala Glu Gly Gly Asp Ser Gly
           130                    135                    140
Gly Ser Phe Ile Ser Gly Asp Gln Ala Gln Gly Val Thr Ser Gly Gly
145                    150                    155                    160
Trp Gly Asn Cys Ser Ser Gly Gly Glu Thr Trp Phe Gln Pro Val Asn
                   165                    170                    175
Glu Ile Leu Asn Arg Tyr Gly Leu Thr Leu His Thr Ala
               180                    185


<210>   43
<211>   197
<212>   PRT
<213>   Rarobacter faecitabidus


<400>   43

Val Ile Val Pro Val Arg Asp Tyr Trp Gly Gly Asp Ala Leu Ser Gly
1                   5                    10                    15
Cys Thr Leu Ala Phe Pro Val Tyr Gly Gly Phe Leu Thr Ala Gly His
               20                    25                    30
Cys Ala Val Glu Gly Lys Gly His Ile Leu Lys Thr Glu Met Thr Gly
           35                    40                    45
```

```
Gly Gln Ile Gly Thr Val Glu Ala Ser Gln Phe Gly Asp Gly Ile Asp
    50                      55                  60
Ala Ala Trp Ala Lys Asn Tyr Gly Asp Trp Asn Gly Arg Gly Arg Val
65                  70                  75                      80
Thr His Trp Asn Gly Gly Gly Val Asp Ile Lys Gly Ser Asn Glu
                85                  90                  95
Ala Ala Val Gly Ala His Met Cys Lys Ser Gly Arg Thr Thr Lys Trp
            100             105                 110
Thr Cys Gly Tyr Leu Leu Arg Lys Asp Val Ser Val Asn Tyr Gly Asn
        115                 120                 125
Gly His Ile Val Thr Leu Asn Glu Thr Ser Ala Cys Ala Leu Gly Gly
    130                 135                 140
Asp Ser Gly Gly Ala Tyr Val Trp Asn Asp Gln Ala Gln Gly Ile Thr
145                 150                 155                     160
Ser Gly Ser Asn Met Asp Thr Asn Asn Cys Arg Ser Phe Tyr Gln Pro
                165                 170                 175
Val Asn Thr Val Leu Asn Lys Trp Lys Leu Ser Leu Val Thr Ser Thr
                180                 185                 190
Asp Val Thr Thr Ser
        195


<210>  44
<211>  191
<212>  PRT
<213>  Streptomyces coelicolor


<400>  44

Asp Pro Pro Leu Arg Ser Gly Leu Ala Ile Tyr Gly Thr Asn Val Arg
1               5                   10                  15
Cys Ser Ser Ala Phe Met Ala Tyr Ser Gly Ser Ser Tyr Tyr Met Met
            20                  25                  30
Thr Ala Gly His Cys Ala Glu Asp Ser Ser Tyr Trp Glu Val Pro Thr
        35                  40                  45
Tyr Ser Tyr Gly Tyr Gln Gly Val Gly His Val Ala Asp Tyr Thr Phe
    50                  55                  60
Gly Tyr Tyr Gly Asp Ser Ala Ile Val Arg Val Asp Asp Pro Gly Phe
65                  70                  75                      80
Trp Gln Pro Arg Gly Trp Val Tyr Pro Ser Thr Arg Ile Thr Asn Trp
            85                  90                  95
Asp Tyr Asp Tyr Val Gly Gln Tyr Val Cys Lys Gln Gly Ser Thr Thr
            100             105                 110
Gly Tyr Thr Cys Gly Gln Ile Thr Glu Thr Asn Ala Thr Val Ser Tyr
        115                 120                 125
Pro Gly Arg Thr Leu Thr Gly Met Thr Trp Ser Thr Ala Cys Asp Ala
    130                 135                 140
Pro Gly Asp Ser Gly Ser Gly Val Tyr Asp Gly Ser Thr Ala His Gly
145                 150                 155                     160
Ile Leu Ser Gly Gly Pro Asn Ser Gly Cys Gly Met Ile His Glu Pro
                165                 170                 175
Ile Ser Arg Ala Leu Ala Asp Arg Gly Val Thr Leu Leu Ala Gly
            180                 185                 190


<210>  45
<211>  20
<212>  DNA
<213>  Artificial Sequence
```

```
<220>
<223>  primer

<400>  45
tgcgccgagc ccggcgactc                                          20

<210>  46
<211>  20
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  46
gagtcgccgg gctcggcgca                                          20

<210>  47
<211>  26
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  47
ttccccggca acgactacgc gtgggt                                   26

<210>  48
<211>  26
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer


<400>  48
acccacgcgt agtcgttgcc ggggaa                                   26

<210>  49
<211>  20
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  49
gccgctgctc gatcgggttc                                          20

<210>  50
<211>  24

<212>  DNA
<213>  Artificial Sequence
```

<220>
<223> primer

<400> 50
gcagttgccg gagccgccgg acgt   24

<210> 51
<211> 14
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic

<220>
<221> misc_feature
<222> (7)..(7)
<223> n is a, c, g, or t

<400> 51
tsggsgncrt ggtt   14

<210> 52
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 52

Leu Arg Met Ile Thr Thr Asp Ser Gly Ser Ser Pro
1   5   10

<210> 53
<211> 555
<212> DNA
<213> Cellulomonas flavigena

<400> 53
gtcgacgtca tcggggggcaa cgcgtactac atcgggtcgc gctcgcggtg ctcgatcggg   60
ttcgcggtcg agggcgggtt cgtcaccgcg gggcactgcg ggcgcgcggg cgcgagcacg   120
tcgtcaccgt cggggacctt ccgcggctcg tcgttccccg gcaacgacta cgcgtgggtc   180
caggtcgcct cgggcaacac gccgcgcggg ctggtgaaca accactcggg cggcacggtg   240
cgcgtcaccg gctcgcagca ggccgcggtc ggctcgtacg tgtgccgatc gggcagcacg   300
acgggatggc ggtgcggcta cgtccgggcg tacaacacga ccgtgcggta cgcggagggc   360
tcggtctcgg gcctcatccg cacgagcgtg tgcgccgagc cgggcgactc cggcggctcg   420
ctggtcgccg gcacgcaggc ccagggcgtc acgtcgggcg ggtccggcaa ctgccgctac   480
gggggcacga cgtacttcca gcccgtgaac gagatcctgc aggaccagcc cgggccgtcg   540
accacgcgtg ccctа   555

<210> 54
<211> 185

<212> PRT
<213> Cellulomonas flavigena

<400> 54

Val Asp Val Ile Gly Gly Asn Ala Tyr Tyr Ile Gly Ser Arg Ser Arg
1   5   10   15
Cys Ser Ile Gly Phe Ala Val Glu Gly Gly Phe Val Thr Ala Gly His
            20   25   30
Cys Gly Arg Ala Gly Ala Ser Thr Ser Ser Pro Ser Gly Thr Phe Arg
            35   40   45
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Gln Val Ala Ser
        50   55   60
Gly Asn Thr Pro Arg Gly Leu Val Asn Asn His Ser Gly Gly Thr Val
65   70   75   80
Arg Val Thr Gly Ser Gln Gln Ala Ala Val Gly Ser Tyr Val Cys Arg
                85   90   95
Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly Tyr Val Arg Ala Tyr Asn
            100   105   110
Thr Thr Val Arg Tyr Ala Glu Gly Ser Val Ser Gly Leu Ile Arg Thr
            115   120   125
Ser Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Val Ala Gly
        130   135   140
Thr Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Tyr
145   150   155   160
Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ile Leu Gln Asp Gln
                165   170   175
Pro Gly Pro Ser Thr Thr Arg Ala Leu
            180   185

<210> 55
<211> 1009
<212> DNA
<213> Cellulomonas biazotea

<400> 55
taaaacagac ggccagtgaa tttgtaatac gactcactat aggcgaattg aatttagcgg   60
ccgcgaattc gcccttacct atagggcacg cgtggtcgac ggccctgggc tggtacgtcg   120
acgtcactac caacacggtc gtcgtcaacg ccaccgccct cgccgtggcc caggcgaccg   180
agatcgtcgc cgccgcaacg gtgcccgccg acgccgtccg ggtcgtcgag accaccgagg   240
cgccccgcac gttcatcgac gtcatcggcg gcaaccgtta ccggatcaac aacacctcgc   300
gctgctcggt cggcttcgcc gtcagcggcg gcttcgtcac cgccgggcac tgcggcacga   360
ccggcgcgac cacgacgaaa ccgtccggca cgttcgccgg ctcgtcgttc cccggcaacg   420
actacgcgtg ggtgcgcgtc gcgtccggca cacccggt cggcgccgtg aacaactaca   480
gcggcggcac cgtggccgtc gccggctcga cgcaggcgac cgtcggtgcg tccgtctgcc   540
gctccggctc caccacgggg tggcgctgcg gacgatcca ggcgttcaac tccaccgtca   600
actacgcgca gggcagcgtc tccggcctca tccgcacgaa cgtgtgcgcc gagcccggcg   660
actccggcgg ctcgctcatc gccggcaacc aggcccaggg cctgacgtcc ggcgggtcgg   720
gcaactgcac caccggcggg acgacgtact tccagcccgt caacgaggcg ctctccgcct   780
acggcctgac gctcgtcacg tcgtccggcg gcggcggtgg cggcggcacg acctgcaccg   840
ggtacgcgcg gacctacacc ggctcgctcg cctcgcggca gtccgccgtc cagccgtccg   900
gcagctatgt gaccgtcggg tccagcggca ccatccgcgt ctgcctcgac ggcccgagcg   960
ggacggactt cgacctgtac ctgcagaagt ggaacgggtc cgcgtgggc   1009

<210> 56
<211> 335
<212> PRT

<213>   Cellulomonas biazotea

<400>   56

```
Lys Gln Thr Ala Ser Glu Phe Val Ile Arg Leu Thr Ile Gly Glu Leu
1               5                   10                  15
Asn Leu Ala Ala Ala Asn Ser Pro Leu Pro Ile Gly His Ala Trp Ser
            20                  25                  30
Thr Ala Leu Gly Trp Tyr Val Asp Val Thr Thr Asn Thr Val Val Val
            35                  40                  45
Asn Ala Thr Ala Leu Ala Val Ala Gln Ala Thr Glu Ile Val Ala Ala
        50                  55                  60
Ala Thr Val Pro Ala Asp Ala Val Arg Val Val Glu Thr Thr Glu Ala
65                  70                  75                  80
Pro Arg Thr Phe Ile Asp Val Ile Gly Gly Asn Arg Tyr Arg Ile Asn
                85                  90                  95
Asn Thr Ser Arg Cys Ser Val Gly Phe Ala Val Ser Gly Gly Phe Val
            100                 105                 110
Thr Ala Gly His Cys Gly Thr Thr Gly Ala Thr Thr Thr Lys Pro Ser
            115                 120                 125
Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val
            130                 135                 140
Arg Val Ala Ser Gly Asn Thr Pro Val Gly Ala Val Asn Asn Tyr Ser
145                 150                 155                 160
Gly Gly Thr Val Ala Val Ala Gly Ser Thr Gln Ala Thr Val Gly Ala
                165                 170                 175
Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly Thr Ile
            180                 185                 190
Gln Ala Phe Asn Ser Thr Val Asn Tyr Ala Gln Gly Ser Val Ser Gly
            195                 200                 205
Leu Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser
        210                 215                 220
Leu Ile Ala Gly Asn Gln Ala Gln Gly Leu Thr Ser Gly Gly Ser Gly
225                 230                 235                 240
Asn Cys Thr Thr Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ala
                245                 250                 255
Leu Ser Ala Tyr Gly Leu Thr Leu Val Thr Ser Ser Gly Gly Gly Gly
            260                 265                 270
Gly Gly Gly Thr Thr Cys Thr Gly Tyr Ala Arg Thr Tyr Thr Gly Ser
            275                 280                 285
Leu Ala Ser Arg Gln Ser Ala Val Gln Pro Ser Gly Ser Tyr Val Thr
    .290                293                 300
Val Gly Ser Ser Gly Thr Ile Arg Val Cys Leu Asp Gly Pro Ser Gly
305                 310                 315                 320
Thr Asp Phe Asp Leu Tyr Leu Gln Lys Trp Asn Gly Ser Ala Trp
            325                 330                 335
```

<210>   57
<211>   474
<212>   DNA
<213>   Cellulomonas fimi

<400>   57
```
gtggacgtga tcggcggcga cgcctactac atcggcggcc gcagccgctg ttcgatcggg      60
ttcgccgtca ccgggggctt cgtgaccgcc gggcactgcg gccgcaccgg cgcggccacg     120
acgagcccgt cgggcacgtt cgccggctcg agcttcccgg gcaacgacta cgcgtgggtg     180
cgggtcgcgt cgggcaacac gcccgtcggc gcggtgaaca actacagcgg cggcacggtc     240
```

```
gccgtcgccg gctcgaccca ggccgccgtc ggtgcgaccg tgtgccgctc gggctccacc      300
accggctggc ggtgcggcac catccaggcg ttcaacgcga ccgtcaacta cgccgagggc      360
agcgtctccg gcctcatccg cacgaacgtg tgcgccgagc ccggcgactc gggcgggctcg     420
ctcgtcgccg gcaaccaggc gcagggcatg acgtccggcg gctccgacaa ctgc            474
```

<210> 58
<211> 144
<212> PRT
<213> Cellulomonas fimi

<400> 58

```
Val Asp Val Ile Gly Gly Asp Ala Tyr Tyr Ile Gly Gly Arg Ser Arg
1               5                   10                  15
Cys Ser Ile Gly Phe Ala Val Thr Gly Gly Phe Val Thr Ala Gly His
            20                  25                  30
Cys Gly Arg Thr Gly Ala Ala Thr Thr Ser Pro Ser Gly Thr Phe Ala
            35                  40                  45
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Arg Val Ala Ser
        50                  55                  60
Gly Asn Thr Pro Val Gly Ala Val Asn Asn Tyr Ser Gly Gly Thr Val
65                  70                  75                  80
Ala Val Ala Gly Ser Thr Gln Ala Ala Val Gly Ala Thr Val Cys Arg
                85                  90                  95
Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly Thr Ile Gln Ala Phe Asn
            100                 105                 110
Ala Thr Val Asn Tyr Ala Glu Gly Ser Val Ser Gly Leu Ile Arg Thr
            115                 120                 125
Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Val Ala Gly
    130                 135                 140
```

<210> 59
<211> 462
<212> DNA
<213> Cellulomonas gelida

<400> 59
```
ctcgcgggca accaggcgca gggcgtgacg tcgggcgggt cgggcaactg ctcgtcgggc       60
gggacgacgt acttccagcc cgtcaacgag gccctccggg tgtacgggct cacgctcgtg      120
acctctgacg gtgggggcac cgagccgccg ccgaccgggt gccagggcta tgcgcggacc      180
taccagggca gcgtctcggc cgggacgtcg gtcgcgcagc cgaacggttc gtacgtcacg      240
accgggggcg ggacgcaccg ggtgtgcctg agcggaccgg cgggcacgga cctggacctg      300
tacctgcaga agtggaacgg gtactcgtgg ccagcgtcg cgcagtcgac gtcgcctggt       360
gccacggagg cggtcacgta caccgggacc gccggctact accgctacgt ggtccacgcg      420
tacgcgggtt cggggggcgta caccctgggg gcgacgaccc cg                        462
```

<210> 60
<211> 154
<212> PRT
<213> Cellulomonas gelida

<400> 60
```
Leu Ala Gly Asn Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn
1               5                   10                  15
Cys Ser Ser Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ala Leu
            20                  25                  30
Arg Val Tyr Gly Leu Thr Leu Val Thr Ser Asp Gly Gly Gly Thr Glu
```

```
                35                      40                      45
Pro Pro Pro Thr Gly Cys Gln Gly Tyr Ala Arg Thr Tyr Gln Gly Ser
      50                      55                      60
Val Ser Ala Gly Thr Ser Val Ala Gln Pro Asn Gly Ser Tyr Val Thr
65                      70                      75                      80
Thr Gly Gly Gly Thr His Arg Val Cys Leu Ser Gly Pro Ala Gly Thr
                    85                      90                      95
Asp Leu Asp Leu Tyr Leu Gln Lys Trp Asn Gly Tyr Ser Trp Ala Ser
                100                     105                     110
Val Ala Gln Ser Thr Ser Pro Gly Ala Thr Glu Ala Val Thr Tyr Thr
                115                     120                     125
Gly Thr Ala Gly Tyr Tyr Arg Tyr Val Val His Ala Tyr Ala Gly Ser
      130                     135                     140
Gly Ala Tyr Thr Leu Gly Ala Thr Thr Pro
145                     150
```

```
<210>  61
<211>  257
<212>  DNA
<213>  Cellulomonas iranensis


<400>  61
ttccccggca acgactacgc gtgggtccag gtcgggtcgg gcgacacccc ccgcggcctg      60
gtcaacaact acgcgggcgg caccgtgcgg gtcaccgggt cgcagcaggc cgcggtcggc     120
gcgtacgtct gccggtcggg cagcacgacg ggctggcgct gcggcaccgt gcaggcctac     180
aacgcgtcgg tccgctacgc cgagggcacc gtctcgggcc tcatccgcac caacgtctgc     240
gccgagcccg gcgactc                                                   257


<210>  62
<211>  85
<212>  PRT
<213>  Cellulomonas iranensis


<400>  62
```

```
Phe Pro Gly Asn Asp Tyr Ala Trp Val Gln Val Gly Ser Gly Asp Thr
1                   5                   10                      15
Pro Arg Gly Leu Val Asn Asn Tyr Ala Gly Gly Thr Val Arg Val Thr
              20                      25                      30
Gly Ser Gln Gln Ala Ala Val Gly Ala Tyr Val Cys Arg Ser Gly Ser
          35                      40                      45
Thr Thr Gly Trp Arg Cys Gly Thr Val Gln Ala Tyr Asn Ala Ser Val
      50                      55                      60
Arg Tyr Ala Glu Gly Thr Val Ser Gly Leu Ile Arg Thr Asn Val Cys
65                      70                      75                      80
Ala Glu Pro Gly Asp
                85
```

```
<210>  63
<211>  904
<212>  DNA
<213>  Cellulomonas cellasea


<400>  63
gtcgggcggg tccggcaact gccgctacgg gggcacgacg tacttccagc ccgtgaacga      60
gatcctgcag gcctacggtc tgcgtctcgt cctgggctga cacgctcgcg gcgggcccgg     120
ctcgacgcgg ccggcccgtc ggcccgggtc gccgcctggt acgtcgacgt gccgaccaac     180
```

```
aagctcgtcg tcgagtcggt cggcgacacc gcggcggccg ccgacgccgt cgccgccgcg    240
ggcctgcctg ccgacgccgt gacgctcgcg accaccgagg cgccacggac gttcgtcgac    300
gtcatcggcg gcaacgcgta ctacatcaac gcgagcagcc gctgctcggt cggcttcgcg    360
gtcgagggcg ggttcgtcac cgcgggccac tgcgggcgcg cgggcgcgag cacgtcgtca    420
ccgtcgggga ccttccgcgg ctcgtcgttc cccggcaacg actacgcgtg ggtccaggtc    480
gcctcgggca cacgccgcg cgggctggtg aacaaccact cgggcggcac ggtgcgcgtc    540
accggctcgc agcaggccgc ggtcggctcg tacgtgtgcc gatcgggcag cacgacggga    600
tggcggtgcg gctacgtccg ggcgtacaac acgaccgtgc ggtacgcgga gggctcggtc    660
tcgggcctca tccgcacgag cgtgtgcgcc gagccgggcg actccggcgg ctcgctggtc    720
gccggcacgc aggcccaggg cgtcacgtcg ggcgggtccg gcaactgccg ctacggggggc    780
acgacgtact tccagcccgt gaacgagatc ctgcaggcct acggtctgcg tctcgtcctg    840
ggctgacacg ctcgcggcgg gccctcccct gcccgtcgcg cgccggcccc accagcccgg    900
gccg                                                                904


<210>   64
<211>   300
<212>   PRT
<213>   Cellulomonas cellasea


<400>   64

Val Gly Arg Val Arg Gln Leu Pro Leu Arg Gly His Asp Val Leu Pro
1               5                   10                  15
Ala Arg Glu Arg Asp Pro Ala Gly Leu Arg Ser Ala Ser Arg Pro Gly
            20                  25                  30
Leu Thr Arg Ser Arg Arg Ala Arg Leu Asp Ala Ala Gly Pro Ser Ala
            35                  40                  45
Arg Val Ala Ala Trp Tyr Val Asp Val Pro Thr Asn Lys Leu Val Val
        50                  55                  60
Glu Ser Val Gly Asp Thr Ala Ala Ala Asp Ala Val Ala Ala Ala
65                  70                  75                  80
Gly Leu Pro Ala Asp Ala Val Thr Leu Ala Thr Thr Glu Ala Pro Arg
                85                  90                  95
Thr Phe Val Asp Val Ile Gly Gly Asn Ala Tyr Tyr Ile Asn Ala Ser
            100                 105                 110
Ser Arg Cys Ser Val Gly Phe Ala Val Glu Gly Gly Phe Val Thr Ala
        115                 120                 125
Gly His Cys Gly Arg Ala Gly Ala Ser Thr Ser Ser Pro Ser Gly Thr
    130                 135                 140
Phe Arg Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Gln Val
145                 150                 155                 160
Ala Ser Gly Asn Thr Pro Arg Gly Leu Val Asn Asn His Ser Gly Gly
                165                 170                 175
Thr Val Arg Val Thr Gly Ser Gln Gln Ala Ala Val Gly Ser Tyr Val
            180                 185                 190
Cys Arg Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly Tyr Val Arg Ala
        195                 200                 205
Tyr Asn Thr Thr Val Arg Tyr Ala Glu Gly Ser Val Ser Gly Leu Ile
    210                 215                 220
Arg Thr Ser Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Val
225                 230                 235                 240
Ala Gly Thr Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys
                245                 250                 255
Arg Tyr Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ile Leu Gln
            260                 265                 270
Ala Tyr Gly Leu Arg Leu Val Leu Gly His Ala Arg Gly Gly Pro Ser
        275                 280                 285
```

Pro Ala Arg Arg Ala Pro Ala Pro Pro Ala Arg Ala
    290   295   300

<210> 65
<211> 429
<212> DNA
<213> Cellulomonas xylanilytica

<400> 65
cgctgctcga tcgggttcgc cgtgacgggc ggcttcgtga ccgccggcca ctgcggacgg   60
tccggcgcga cgacgacgtc gccgagcggc acgttcgccg ggtccagctt tcccggcaac   120
gactacgcct gggtccgcgc ggcctcgggc aacacgccgg tcggtgcggt gaaccgctac   180
gacggcagcc gggtgaccgt ggccgggtcc accgacgcgg ccgtcggtgc cgcggtctgc   240
cggtcggggt cgacgaccgc gtggggctgc ggcacgatcc agtcccgcgg cgcgagcgtc   300
acgtacgccc agggcaccgt cagcgggctc atccgcacca acgtgtgcgc cgagccgggt   360
gactccgggg ggtcgctgat cgcgggcacc caggcgcggg gcgtgacgtc cggcggctcc   420
ggcaactgc   429

<210> 66
<211> 143
<212> PRT
<213> Cellulomonas xylanilytica

<400> 66

Arg Cys Ser Ile Gly Phe Ala Val Thr Gly Gly Phe Val Thr Ala Gly
1   5   10   15
His Cys Gly Arg Ser Gly Ala Thr Thr Thr Ser Pro Ser Gly Thr Phe
            20   25   30
Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Arg Ala Ala
            35   40   45
Ser Gly Asn Thr Pro Val Gly Ala Val Asn Arg Tyr Asp Gly Ser Arg
            50   55   60
Val Thr Val Ala Gly Ser Thr Asp Ala Ala Val Gly Ala Ala Val Cys
65   70   75   80
Arg Ser Gly Ser Thr Thr Ala Trp Gly Cys Gly Thr Ile Gln Ser Arg
                85   90   95
Gly Ala Ser Val Thr Tyr Ala Gln Gly Thr Val Ser Gly Leu Ile Arg
            100   105   110
Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Ile Ala
            115   120   125
Gly Thr Gln Ala Arg Gly Val Thr Ser Gly Gly Ser Gly Asn Cys
    130   135   140

<210> 67
<211> 1284
<212> DNA
<213> Oerskovia turbata

<400> 67
atggcacgat cattctggag gacgctcgcc acggcgtgcg ccgcgacggc actggttgcc   60
ggccccgcag cgctcaccgc gaacgccgcg acgcccaccc ccgacacccc gaccgtttca   120
ccccagacct cctcgaaggt ctcgcccgag gtgctccgcg ccctccagcg ggacctgggg   180
ctgagcgcca aggacgcgac gaagcgtctg gcgttccagt ccgacgcggc gagcaccgag   240
gacgctctcg ccgacagcct ggacgcctac gcgggcgcct gggtcgaccc tgcgaggaac   300
accctgtacg tcggcgtcgc cgacagggcc gaggccaagg aggtccgttc ggccggagcg   360
accccgtgg tcgtcgacca cacgctcgcc gagctcgaca cgtggaaggc ggcgctcgac   420

```
ggtgagctca acgaccccgc gggcgtcccg agctggttcg tcgacgtcac gaccaaccag    480
gtcgtcgtca acgtgcacga cggcggacgc gccctcgcgg agctggctgc cgcgagcgcg    540
ggcgtgcccg ccgacgccat cacctacgtg acgacgaccg aggctcctcg tcccctcgtc    600
gacgtggtgg cggcaacgc gtacaccatg ggttcgggcg ggcgctgctc ggtcggcttc    660
gcggtgaacg ggggcttcat cacggccggg cactgcggct cggtcggcac ccgcacctcg    720
gggccgggcg cacgttccg ggggtcgaac ttccccggca acgactacgc ctgggtgcag    780
gtcgacgcgg gtaacacccc ggtcggcgcg gtcaacaact acagcggtgg gcgcgtcgcg    840
gtcgcagggt cgacggccgc gcccgtgggg gcctcggtct gccggtccgg ttccacgacg    900
ggctggcact gcggcaccat cggcgcgtac aacacctcgg tgacgtaccc gcagggcacc    960
gtctcggggc tcatccgcac gaacgtgtgc gccgagcccg gcgactcggg cggctcgctc    1020
ctcgcgggca accaggcgca gggcgtgacc tcgggcgggt cgggcaactg ctcgtcgggc    1080
gggacgacgt acttccagcc cgtcaacgag gccctcgggg ggtacgggct cacgctcgtg    1140
acctctgacg gtggggggccc gagccgccgc cgaccgggtg ccagggctat gcgcggacct    1200
accagggcag cgtctcggcc gggacgtcgg tcgcgcagcg aacggttcgt acgtcacgac    1260
cggggggcggg cgaccgggtg tgcc                                          1284
```

<210> 68
<211> 428
<212> PRT
<213> Oerskovia turbata

<400> 68

```
Met Ala Arg Ser Phe Trp Arg Thr Leu Ala Thr Ala Cys Ala Ala Thr
1               5                   10                  15
Ala Leu Val Ala Gly Pro Ala Ala Leu Thr Ala Asn Ala Ala Thr Pro
            .20                  25                  30
Thr Pro Asp Thr Pro Thr Val Ser Pro Gln Thr Ser Ser Lys Val Ser
        35                  40                  45
Pro Glu Val Leu Arg Ala Leu Gln Arg Asp Leu Gly Leu Ser Ala Lys
    50                  55                  60
Asp Ala Thr Lys Arg Leu Ala Phe Gln Ser Asp Ala Ala Ser Thr Glu
65                  70                  75                  80
Asp Ala Leu Ala Asp Ser Leu Asp Ala Tyr Ala Gly Ala Trp Val Asp
                85                  90                  95
Pro Ala Arg Asn Thr Leu Tyr Val Gly Val Ala Asp Arg Ala Glu Ala
            100                 105                 110
Lys Glu Val Arg Ser Ala Gly Ala Thr Pro Val Val Val Asp His Thr
        115                 120                 125
Leu Ala Glu Leu Asp Thr Trp Lys Ala Ala Leu Asp Gly Glu Leu Asn
    130                 135                 140
Asp Pro Ala Gly Val Pro Ser Trp Phe Val Asp Val Thr Thr Asn Gln
145                 150                 155                 160
Val Val Val Asn Val His Asp Gly Gly Arg Ala Leu Ala Glu Leu Ala
                165                 170                 175
Ala Ala Ser Ala Gly Val Pro Ala Asp Ala Ile Thr Tyr Val Thr Thr
            180                 185                 190
Thr Glu Ala Pro Arg Pro Leu Val Asp Val Val Gly Gly Asn Ala Tyr
        195                 200                 205
Thr Met Gly Ser Gly Gly Arg Cys Ser Val Gly Phe Ala Val Asn Gly
    210                 215                 220
Gly Phe Ile Thr Ala Gly His Cys Gly Ser Val Gly Thr Arg Thr Ser
225                 230                 235                 240
Gly Pro Gly Gly Thr Phe Arg Gly Ser Asn Phe Pro Gly Asn Asp Tyr
                245                 250  .              255
Ala Trp Val Gln Val Asp Ala Gly Asn Thr Pro Val Gly Ala Val Asn
            260                 265                 270
```

```
Asn Tyr Ser Gly Gly Arg Val Ala Val Ala Gly Ser Thr Ala Ala Pro
        275                 280                 285
Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys
        290                 295                 300
Gly Thr Ile Gly Ala Tyr Asn Thr Ser Val Thr Tyr Pro Gln Gly Thr
305                 310                 315                 320
Val Ser Gly Leu Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser
                325                 330                 335
Gly Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val Thr Ser Gly
                340                 345                 350
Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Tyr Phe Gln Pro Val
                355                 360                 365
Asn Glu Ala Leu Gly Gly Tyr Gly Leu Thr Leu Val Thr Ser Asp Gly
        370                 375                 380
Gly Gly Pro Ser Arg Arg Arg Pro Gly Ala Arg Ala Met Arg Gly Pro
385                 390                 395                 400
Thr Arg Ala Ala Ser Arg Pro Gly Arg Arg Ser Arg Ser Glu Arg Phe
                405                 410                 415
Val Arg His Asp Arg Gly Arg Ala Thr Gly Cys Ala
                420                 425
```

<210> 69
<211> 524
<212> DNA
<213> Oerskovia jenensis

<400> 69
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gccgctgctc ggtcggcttc gcggtgaacg gcggcttcgt caccgcaggc cactgcggga    60
cggtgggcac ccgcacctcg gggccgggcg gcacgttccg cgggtcgagc ttccccggca   120
acgactacgc ctgggtgcag gtcgacgcgg ggaacacccc ggtcggggcc gtcaacaact   180
acagcggtgg acgcgtcgcg gtcgcgggct cgacggccgc acccgtgggt tcctcggtct   240
gccggtccgg ttccacgacg ggctggcgct gcggcacgat cgcggcctac aacagctcgg   300
tgacgtaccc gcaggggacc gtctccgggc tcatccgcac caacgtgtgc gccgagccgg   360
gcgactcggg cggctcgctc ctcgcgggca accaggcaca gggcctgacg tcgggcgggt   420
cgggcaactg ctcgtcgggc ggcacgacgt acttccagcc cgtcaacgag gcgctctcgg   480
cctacggcct cacgctcgtg acctccggcg cagggggcaa ctgc                    524
                                                                     ｀
```

<210> 70
<211> 174
<212> PRT
<213> Oerskovia jenensis

<400> 70

```
Arg Cys Ser Val Gly Phe Ala Val Asn Gly Gly Phe Val Thr Ala Gly
1                 5                  10                  15
His Cys Gly Thr Val Gly Thr Arg Thr Ser Gly Pro Gly Gly Thr Phe
            20                  25                  30
Arg Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Gln Val Asp
            35          .       40                  45
Ala Gly Asn Thr Pro Val Gly Ala Val Asn Asn Tyr Ser Gly Gly Arg
        50                  55                  60
Val Ala Val Ala Gly Ser Thr Ala Ala Pro Val Gly Ser Ser Val Cys
65                  70                  75                  80
Arg Ser Gly Ser Thr Thr Gly Trp Arg Cys Gly Thr Ile Ala Ala Tyr
                85                  90                  95
Asn Ser Ser Val Thr Tyr Pro Gln Gly Thr Val Ser Gly Leu Ile Arg
```

```
                100                    105                    110
Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala


                115                    120                    125
Gly Asn Gln Ala Gln Gly Leu Thr Ser Gly Gly Ser Gly Asn Cys Ser
    130                    135                    140
Ser Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ala Leu Ser Ala
145                    150                    155                    160
Tyr Gly Leu Thr Leu Val Thr Ser Gly Gly Arg Gly Asn Cys
                    165                    170
```

```
<210>  71
<211>  984
<212>  DNA
<213>  Cellulosimicrobium cellulans

<400>  71
ccacgggcgg cgggtcgggc agcgcgctcg tcgggctcgc gggcaagtgc atcgacgtcc      60
ccgggtccga cttcagtgac ggcaagcgcc tccagctgtg gacgtgcaac gggtcgcagg     120
cagcgctgga cgttcgaagc cgacggcacc gtacgcgcgg cggcaagtg catggacgtc     180
gcgtgggcgc cgcggccgac ggcacggcgc tccagctcgc gaactgcacg gcaacgcggc     240
ccagaagttc gtgctcaacg gcgcgggcga cctcgtgtcg gtgctggcga caaagtgcg     300
tcgacgccgc cgggtgcgca ccgaggtact cgcggcgccg tacgagctca cggcgacgtg     360
cgcggcggcg accgctacat cacacgggac ccgggcgcgt cgtcgggctc ggcctgctcg     420
atcgggtacg ccgtccaggg cggcttcgtc acggcggggc actgcggacg cggcgggaca     480
aggagagtgc tcaccgcgag ctgggcgcgc atggggacgg tccaggcggc gtcgttcccc     540
ggccacgact acgcgtgggt gcgcgtcgac gccgggttct cccccgtccc gcgggtgaac     600
aactacgccg cggcaccgt cgacgtcgcc ggctcggccg aggcgcccgt gggtgcgtcg     660
gtgtgccgct cgggcgccac gaccggctgg cgctgcggcg tcatcgagca gaagaacatc     720
accgtcaact acggcaacgg cgacgttccc ggcctcgtgc gcggcagcgc gtgcgcggag     780
ggcggcgact cgggcgggtc ggtgatctcc ggcaaccagg cgcagggcgt cacgtcgggc     840
aggatcaacg actgctcgaa cggcggcaag ttcctctacc agcccgatcg acggcctgtc     900
gctcgtgacc acgggcggcg ggtcgggcag cgcgctcgtc gggctcgcgg gcaagtgcat     960
cgacgtcccc gggtccgact tcag                                            984
```

```
<210>  72

<211>  328
<212>  PRT
<213>  Cellulosimicrobium cellulans

<400>  72

Pro Arg Ala Ala Gly Arg Ala Ala Arg Ser Ser Gly Ser Arg Ala Ser
1               5                   10                  15
Ala Ser Thr Ser Pro Gly Pro Thr Ser Val Thr Ala Ser Ala Ser Ser
                20                  25                  30
Cys Gly Arg Ala Thr Gly Arg Arg Gln Arg Trp Thr Phe Glu Ala Asp
            35                  40                  45
Gly Thr Val Arg Ala Gly Gly Lys Cys Met Asp Val Ala Trp Ala Pro
        50                  55                  60
Arg Pro Thr Ala Arg Arg Ser Ser Ser Arg Thr Ala Arg Gln Arg Gly
65                  70                  75                  80
Pro Glu Val Arg Ala Gln Arg Arg Gly Arg Pro Arg Val Gly Ala Gly
                85                  90                  95
Glu Gln Ser Ala Ser Thr Pro Pro Gly Ala His Arg Gly Thr Arg Gly
```

```
                100                   105                   110
Ala Val Arg Ala His Gly Asp Val Arg Gly Gly Asp Arg Tyr Ile Thr
        115                   120                   125
Arg Asp Pro Gly Ala Ser Ser Gly Ser Ala Cys Ser Ile Gly Tyr Ala
    130                   135                   140
Val Gln Gly Gly Phe Val Thr Ala Gly His Cys Gly Arg Gly Gly Thr
145                   150                   155                   160
Arg Arg Val Leu Thr Ala Ser Trp Ala Arg Met Gly Thr Val Gln Ala
                165                   170                   175
Ala Ser Phe Pro Gly His Asp Tyr Ala Trp Val Arg Val Asp Ala Gly
            180                   185                   190
Phe Ser Pro Val Pro Arg Val Asn Asn Tyr Ala Gly Gly Thr Val Asp
            195                   200                   205
Val Ala Gly Ser Ala Glu Ala Pro Val Gly Ala Ser Val Cys Arg Ser
    210                   215                   220
Gly Ala Thr Thr Gly Trp Arg Cys Gly Val Ile Glu Gln Lys Asn Ile
225                   230                   235                   240
Thr Val Asn Tyr Gly Asn Gly Asp Val Pro Gly Leu Val Arg Gly Ser
                245                   250                   255
Ala Cys Ala Glu Gly Gly Asp Ser Gly Gly Ser Val Ile Ser Gly Asn
            260                   265                   270
Gln Ala Gln Gly Val Thr Ser Gly Arg Ile Asn Asp Cys Ser Asn Gly
        275                   280                   285
Gly Lys Phe Leu Tyr Gln Pro Asp Arg Arg Pro Val Ala Arg Asp His
    290                   295                   300
Gly Arg Arg Val Gly Gln Arg Ala Arg Arg Ala Arg Gly Gln Val His
305                   310                   315                   320
Arg Arg Pro Arg Val Arg Leu Gln
                325


<210>  73
<211>  257
<212>  DNA
<213>  Promicromonospora citrea


<400>  73
ttccccggca acgactacgc gtgggtgaac acgggcacgg acgacaccct cgtcggcgcc      60
gtgaacaact acagcggcgg cacggtcaac gtcgcgggct cgacccgtgc cgccgtcggc     120
gcgacggtct gccgctcggg ctccacgacc ggctggcact gcggcaccat ccaggcgctg     180
aacgcgtcgg tcacctacgc cgagggcacc gtgagcggcc tcatccgcac caacgtgtgc     240
gccgagcccg gcgactc                                                    257


<210>  74
<211>  85
<212>  PRT
<213>  Promicromonospora citrea


<400>  74

Phe Pro Gly Asn Asp Tyr Ala Trp Val Asn Thr Gly Thr Asp Asp Thr
1                   5                   10                  15
Leu Val Gly Ala Val Asn Asn Tyr Ser Gly Gly Thr Val Asn Val Ala
            20                  25                  30
Gly Ser Thr Arg Ala Ala Val Gly Ala Thr Val Cys Arg Ser Gly Ser
        35                  40                  45
Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Leu Asn Ala Ser Val
    50                  55                  60
```

Thr Tyr Ala Glu Gly Thr Val Ser Gly Leu Ile Arg Thr Asn Val Cys
65   70   75   80
Ala Glu Pro Gly Asp
                85

<210>   75
<211>   257
<212>   DNA
<213>   Promicromonospora sukumoe

<400>   75
ttccccggca acgactacgc gtgggtgaac gtcggctccg acgacacccc gatcggtgcg   60
gtcaacaact acagcggcgg caccgtgaac gtcgcgggct cgacccaggc cgccgtcggc   120
tccaccgtct gccgctccgg ttccacgacc ggctggcact gcggcaccat ccaggccttc   180
aacgcgtcgg tcacctacgc cgagggcacc gtgtccggcc tgatccgcac caacgtctgc   240
gccgagcccg gcgactc   257

<210>   76
<211>   85
<212>   PRT
<213>   Promicromonospora sukumoe

<400>   76

Phe Pro Gly Asn Asp Tyr Ala Trp Val Asn Val Gly Ser Asp Asp Thr
1   5   10   15
Pro Ile Gly Ala Val Asn Asn Tyr Ser Gly Gly Thr Val Asn Val Ala
                20   25   30
Gly Ser Thr Gln Ala Ala Val Gly Ser Thr Val Cys Arg Ser Gly Ser
            35   40   45
Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Phe Asn Ala Ser Val
        50   55   60
Thr Tyr Ala Glu Gly Thr Val Ser Gly Leu Ile Arg Thr Asn Val Cys
65   70   75   80
Ala Glu Pro Gly Asp
                85

<210>   77
<211>   430
<212>   DNA
<213>   Xylanibacterium ulmi

<400>   77
gccgctgctc gatcgggttc gccgtgacgg gcggcttcgt gaccgccggc cactgcggac   60
ggtccggcgc gacgacgacg tccgcgagcg gcacgttcgc cgggtccagc tttcccggca   120
acgactacgc ctgggtccgc gcggcctcgg aacacgccg gtcggtgcgg tgaaccgcta   180
cgacggcagc cgggtgaccg tggccgggtc caccgacgcg ccgtcggtg ccgcggtctg   240
ccggtcgggg tcgacgaccg cgtggcgctg cggcacgatc cagtcccgcg cgcgacggt   300
cacgtacgcc cagggcaccg tcagcgggct catccgcacc aacgtgtgcg ccgagccggg   360
tgactccggg gggtcgctga tcgcgggcac ccaggcgcag ggcgtgacgt ccggcggctc   420
cggcaactgc   430

<210>   78
<211>   141
<212>   PRT
<213>   Xylanibacterium ulmi

<400> 78

```
Arg Cys Ser Ile Gly Phe Ala Val Thr Gly Gly Phe Val Thr Ala Gly
1               5                   10                  15
His Cys Gly Arg Ser Gly Ala Thr Thr Thr Ser Ala Ser Gly Thr Phe
            20                  25                  30
Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Trp Val Arg Ala Ala
            35                  40                  45
Ser Gly Asn Thr Pro Val Gly Ala Val Asn Arg Tyr Asp Gly Ser Arg
        50                  55                  60
Val Thr Val Ala Gly Ser Thr Asp Ala Ala Val Gly Ala Ala Val Cys
65                  70                  75                  80
Arg Ser Gly Ser Thr Thr Ala Trp Arg Cys Gly Thr Ile Gln Ser Arg
                85                  90                  95
Gly Ala Thr Val Thr Tyr Ala Gln Gly Thr Val Ser Gly Leu Ile Arg
                100                 105                 110
Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Ile Ala
            115                 120                 125
Gly Thr Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly
        130                 135                 140
```

<210> 79

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 79
acccacgcgt agtcgttgcc   20

<210> 80
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 80
acccacgcgt agtcgtkgcc gggg   24

<210> 81
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 81
tcgtcgtggt cgcgccgg   18

<210> 82
<211> 17

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<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   82
cgacgtgctc gcgcccg                                                      17

<210>   83
<211>   18
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   83
cgcgcccagc tcgcggtg                                                     18

<210>   84
<211>   22
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   84
cggccccgag gtgcgggtgc cg                                                22

<210>   85
<211>   22
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   85
cagcgtctcc ggcctcatcc gc                                                22

<210>   86
<211>   22
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   86
ctcggtctcg ggcctcatcc gc                                                22

<210>   87
<211>   22
<212>   DNA
<213>   Artificial Sequence
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<220>
<223> primer

<400> 87
cgacgttccc ggcctcgtgc gc   22

<210> 88
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 88
caccgtctcg gggctcatcc gc   22

<210> 89
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 89
agcarcgtgt gcgccgagcc   20

<210> 90
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 90
ggcagcgcgt gcgcggaggg   20

<210> 91
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 91
gccgctgctc gatcgggttc   20

<210> 92
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<400> 92
gcagttgccg gagccgccgg acgt   24

<210> 93
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 93
tgcgccgagc ccggcgactc cggc   24

<210> 94
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 94
ggcacgacgt acttccagcc cgtgaac   27

<210> 95
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 95
gacccacgcg tagtcgttgc cggggaacga cga   33

<210> 96
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 96
gaaggtcccc gacggtgacg acgtgctcgc gcc   33

<210> 97
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

```
<400>  97
caggcgcagg gcgtgacctc gggcgggtcg                                    30


<210>  98
<211>  29
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  98
ggcgggacga cgtacttcca gcccgtcaa                                     29


<210>  99
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  99
cacccacgcg tagtcgtggc cggggaacga                                    30


<210>  100
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  100
gaagccgccc tggacggcgt acccgatcga gca                                33


<210>  101
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  101
tgcgcggagg gcggcgactc gggcgggtcg                                    30


<210>  102
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  102
ttcctctacc agcccgtcaa cccgatccta                                    30
```

```
<210>  103
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  103
cgccgcgggg acgaacccgc cctcgaccgc gaa                                    33

<210>  104
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  104
cgcgtagtcg ttgccgggga acgacgagcc                                        30

<210>  105
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  105
ggcctcatcc gcacgagcgt gtgcgccgag                                        30

<210>  106
<211>  36
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer


<400>  106
acgtcgggcg ggtccggcaa ctgccgctac gggggc                                 36

<210>  107
<211>  39
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  107
gagcccgtac acccggaggg cctcgttgac gggctggaa                              39
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<210>   108
<211>   30
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   108
cgtcacgccc tgcgcctggt tgcccgcgag                              30

<210>   109
<211>   38
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   109
tccagcccgt caacgaggcc ctccgggtgt acgggctc                     38

<210>   110
<211>   33
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   110
acgtcggtcg cgcagccgaa cggttcgtac gtc                          33

<210>   111
<211>   30

<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   111
cgtggtcgcg ccggtcgtgc cgcagtgccc                              30

<210>   112
<211>   36
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   112
gacgacgacc gtgttggtag tgacgtcgac gtacca                       36

<210>   113
```

```
<211>   30
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   113
tccaccacgg ggtggcgctg cgggacgatc                                        30

<210>   114
<211>   30
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   114
gtgtgcgccg agcccggcga ctccggcggc                                        30

<210>   115
<211>   36
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   115
gctcgggccc ccaccgtcag aggtcacgag cgtgag                                 36

<210>   116
<211>   36
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   116
atggcacgat cattctggag gacgctcgcc acggcg                                 36

<210>   117
<211>   33
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   117
tgctcgatcg ggtacgccgt ccagggcggc ttc                                    33

<210>   118
<211>   30
<212>   DNA
```

<213> Artificial Sequence

<220>
<223> primer

<400> 118
taggatcggg ttgacgggct ggtagaggaa   30

<210> 119
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 119
tggtacgtcg acgtcactac caacacggtc gtcgtc   36

<210> 120
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 120
gccgccggag tcgccgggct cggcgcacac   30

<210> 121
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 121
gtsgacgtsa tcggsggsaa cgcstactac   30

<210> 122
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<220>
<221> misc_feature
<222> (13)..(16)
<223> n is a, c, g, or t

<400> 122
sgcsgtsgcs ggnganga   18

```
<210>  123
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  123
gtsgaygtsa tcggcggcga ygcstac                                              27

<210>  124
<211>  18
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<220>
<221>  misc_feature
<222>  (10)..(16)
<223>  n is a, c, g, or t

<400>  124
sgasgcgtan ccctgncc                                                        18

<210>  125
<211>  189
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  consensus sequence

<220>
<221>  VARIANT
<222>  1, 8-16, 24, 35, 36, 38, 39, 41-44, 48, 61-64, 66, 67, 69-71, 81, 87, 89,
93, 109-111, 113, 116
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  VARIANT
<222>  4, 19, 28, 108, 126
<223>  Xaa is Ile or Val

<220>
<221>  VARIANT
<222>  7, 157
<223>  Xaa is Asn or Asp

<220>

<221>  VARIANT
<222>  92, 99, 143
<223>  Xaa is Ser or Ala
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<220>
<221>   VARIANT
<222>   112, 156
<223>   Xaa is Asn or Gly


<220>
<221>   VARIANT
<222>   21
<223>   Xaa is Phe or Tyr


<220>
<221>   VARIANT
<222>   40
<223>   Xaa is Thr or Val


<220>
<221>   VARIANT
<222>   59
<223>   Xaa is Phe or Trp


<220>
<221>   VARIANT
<222>   65
<223>   Xaa is Gly or Asp


<220>
<221>   VARIANT
<222>   68
<223>   Xaa is Leu or Phe


<220>
<221>   VARIANT
<222>   74
<223>   Xaa is Asn or Arg


<220>
<221>   VARIANT
<222>   75
<223>   Xaa is Tyr or His


<220>
<221>   VARIANT
<222>   76
<223>   Xaa is Ser or Asp


<220>
<221>   VARIANT
<222>   78
<223>   Xaa is Gly or Ser


<220>
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<222>   79
<223>   Xaa is Arg or Thr


<220>
<221>   VARIANT
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<222>  83
<223>  Xaa is Ala or Thr


<220>
<221>  VARIANT
<222>  85
<223>  Xaa is His or Ser


<220>
<221>  VARIANT
<222>  86
<223>  Xaa is Thr or Gln


<220>
<221>  VARIANT
<222>  102
<223>  Xaa is Gly or Ala


<220>
<221>  VARIANT
<222>  104
<223>  Xaa is His or Arg


<220>
<221>  VARIANT
<222>  107
<223>  Xaa is Thr or Tyr


<220>
<221>  VARIANT
<222>  114
<223>  Xaa is Ser or Thr


<220>
<221>  VARIANT
<222>  118
<223>  Xaa is Pro or Ala


<220>
<221>  VARIANT
<222>  119
<223>  Xaa is Glu or Gln


<220>
<221>  VARIANT
<222>  121
<223>  Xaa is Thr, Ser, or Asp


<220>
<221>  VARIANT
<222>  123
<223>  Xaa is Arg or Ser


<220>
<221>  VARIANT
<222>  128
<223>  Xaa is Thr or Gly
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<220>
<221>  VARIANT
<222>  129
<223>  Xaa is Thr, Asn, or Ser

<220>
<221>  VARIANT
<222>  130
<223>  Xaa is Val or Ala

<220>
<221>  VARIANT
<222>  134
<223>  Xaa is Pro or Gly

<220>
<221>  VARIANT
<222>  141
<223>  Xaa is Leu or Val

<220>
<221>  VARIANT
<222>  142
<223>  Xaa is Leu, Val, or Ile

<220>
<221>  VARIANT
<222>  145
<223>  Xaa is Asn or Thr

<220>
<221>  VARIANT
<222>  148
<223>  Xaa is Gln or Arg

<220>
<221>  VARIANT
<222>  150
<223>  Xaa is Val or Leu

<220>
<221>  VARIANT
<222>  154
<223>  Xaa is Gly or Arg

<220>
<221>  VARIANT
<222>  155
<223>  Xaa is Ser or Ile

<220>
<221>  VARIANT
<222>  159, 160, 163-166, 169-189
<223>  Xaa can be any naturally occurring amino acid

<400>  125
```

```
Xaa Asp Val Xaa Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10                  15
Cys Ser Xaa Gly Xaa Ala Val Xaa Gly Gly Phe Xaa Thr Ala Gly His
            20              25              30
Cys Gly Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Thr Phe Xaa
            35              40              45
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Xaa Val Xaa Xaa Xaa Xaa
        50              55              60
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Asn Xaa Xaa Xaa Gly Xaa Xaa Val
65                  70              75                      80
Xaa Val Xaa Gly Xaa Xaa Xaa Ala Xaa Val Gly Xaa Xaa Val Cys Arg
            85              90                      95
Ser Gly Xaa Thr Thr Xaa Trp Xaa Cys Gly Xaa Xaa Xaa Xaa Xaa Xaa
            100             105             110
Xaa Xaa Val Xaa Tyr Xaa Xaa Gly Xaa Val Xaa Gly Leu Xaa Arg Xaa
        115             120             125
Xaa Xaa Cys Ala Glu Xaa Gly Asp Ser Gly Gly Ser Xaa Xaa Xaa Gly
    130             135             140
Xaa Gln Ala Xaa Gly Xaa Thr Ser Gly Xaa Xaa Xaa Xaa Cys Xaa Xaa
145             150             155                     160
Gly Gly Xaa Xaa Xaa Xaa Gln Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            165             170             175
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            180             185
```

```
<210>  126
<211>  16
<212>  PRT
<213>  Cellulomonas cellasea

<220>
<221>  VARIANT
<222>  (1)..(1)
<223>  Xaa is Ile or Tyr

<400>  126

Xaa Ala Trp Asp Ala Phe Ala Glu Asn Val Val Asp Trp Ser Ser Arg
1               5                   10                  15

<210>  127
<211>  17
<212>  PRT
<213>  Cellulomonas cellasea

<400>  127

Tyr Gly Gly Thr Thr Tyr Phe Gln Pro Val Asn Glu Ile Leu Gln Ala
1               5                   10                  15
Tyr


<210>  128
<211>  11
<212>  PRT
<213>  Cellulomonas flavigena
```

<220>
<221> VARIANT
<222> (4)..(11)
<223> Xaa is Ile or Tyr

<400> 128

Val Asp Val Xaa Gly Gly Asn Ala Tyr Tyr Xaa
1   5   10

<210> 129
<211> 9
<212> PRT
<213> Cellulomonas fimi

<220>
<221> VARIANT
<222> (4)..(4)
<223> Xaa is Ile or Tyr

<400> 129

Val Asp Val Xaa Gly Gly Asp Ala Tyr
1   5

<210> 130
<211> 305
<212> DNA
<213> Aspergillus niger

<220>
<221> misc_feature
<222> (186)..(186)
<223> n is a, c, g, or t

<400> 130
tcgaacttca tgttcgagtt cttgttcacg tagaagccgg agatgtgaga ggtgatctgg   60
aactgctcac cctcgttggt ggtgacctgg aggtaaagca agtgaccctt ctggcggagg   120
tggtaaggaa cggggttcca cggggagaga gagatggcct tgacggtctt gggaagggga   180
gcttcngcgc gggggaggat ggtcttgaga gaggggggagc tagtaatgtc gtacttggac   240
agggagtgct ccttctccga cgcatcagcc acctcagcgg agatggcatc gtgcagagac   300
agacc   305

<210> 131
<211> 1488
<212> DNA
<213> Cellulomonas strain 69B4

<400> 131
atgacaccac gaactgtcac aagagctctg gctgtggcaa cagcagctgc tacactcttg   60
gctgggggta tggcagcaca agctaacgaa ccggctcctc caggatctgc atcagcccct   120
ccacgattag ctgaaaaaact tgaccctgac ttacttgaag caatggaacg cgatctgggg   180
ttagatgcag aggaagcagc tgcaacgtta gcttttcagc atgacgcagc tgaaacggga   240
gaggctcttg ctgaggaact cgacgaagat ttcgcgggca cgtgggttga agatgatgtg   300
ctgtatgttg caaccactga tgaagatgct gttgaagaag tcgaaggcga aggagcaact   360
gctgtgactg ttgagcattc tcttgctgat ttagaggcgt ggaagacggt tttggatgct   420

```
gcgctggagg gtcatgatga tgtgcctacg tggtacgtcg acgtgcctac gaattcggta      480
gtcgttgctg taaaggcagg agcgcaggat gtagctgcag gacttgtgga aggcgctgat      540
gtgccatcag atgcggtcac ttttgtagaa acggacgaaa cgcctagaac gatgttcgac      600
gtaattggag gcaacgcata tactattggc ggccggtcta gatgttctat cggattcgca      660
gtaaacggtg gcttcattac tgccggtcac tgcggaagaa caggagccac tactgccaat      720
ccgactggca catttgcagg tagctcgttt ccgggaaatg attatgcatt cgtccgaaca      780
ggggcaggag taaatttgct tgcccaagtc aataactact cgggcggcag agtccaagta      840
gcaggacata cggccgcacc agttggatct gctgtatgcc gctcaggtag cactacaggt      900
tggcattgcg gaactatcac ggcgctgaat cgtctgtca cgtatccaga gggaacagtc       960
cgaggactta tccgcacgac ggtttgtgcc gaaccaggtg atagcggagg tagccttta     1020
gcgggaaatc aagcccaagg tgtcacgtca ggtggttctg gaaattgtcg acggggggga     1080
acaacattct ttcaaccagt caacccgatt ttgcaggctt acggcctgag aatgattacg     1140
actgactctg gaagttcccc tgctccagca cctacatcat gtacaggcta cgcaagaacg     1200
ttcacaggaa ccctcgcagc aggaagagca gcagctcaac cgaacggtag ctatgttcag     1260
gtcaaccgga gcggtacaca ttccgtctgt ctcaatggac ctagcggtgc ggactttgat     1320
ttgtatgtgc agcgatggaa tggcagtagc tgggtaaccg tcgctcaatc gacatcgccg     1380
ggaagcaatg aaaccattac gtaccgcgga aatgctggat attatcgcta cgtggttaac     1440
gctgcgtcag gatcaggagc ttacacaatg ggactcaccc tcccctga               1488
```

<210> 132
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 132

Asp Asp Asn Asp Pro Ile
1   5

<210> 133
<211> 1020
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 133
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gtgagaagca aaaaattgtg gatcagcttg ttgtttgcgt taacgttaat ctttacgatg       60
gcgttcagca acatgagcgc gcaggctgat gattattcag ttgtagagga acatgggcaa      120
ctaagtatta gtaacggtga attagtcaat gaacgaggcg aacaagttca gttaaaaggg      180
atgagttccc atggtttgca atggtacggt caatttgtaa actatgaaag catgaaatgg      240
ctaagagatg attggggaat aactgtattc cgagcagcaa tgtatacctc ttcaggagga      300
tatattgacg atccatcagt aaaggaaaaa gtaaaagaga ctgttgaggc tgcgatagac      360
cttggcatat atgtgatcat tgattggcat atcctttcag caatgaccc gaatatatat       420
aaagaagaag cgaaggattt ctttgatgaa atgtcagagt gtatggaga ctatccgaat       480
gtgatatacg aaattgcaaa tgaaccgaat ggtagtgatg ttacgtggga caatcaaata      540
aaaccgtatg cagaagaagt gattccggtt attcgtgaca atgaccctaa taacattgtt      600
attgtaggta caggtacatg gagtcaggat gtccatcatg cagccgataa tcagcttgca      660
gatcctaacg tcatgtatgc atttcatttt tatgcaggaa cacatggaca aaatttacga      720
gaccaagtag attatgcatt agatcaagga gcagcgatat ttgttagtga atgggggaca      780
agtgcagcta caggtgatgg tggtgtgttt ttagatgaag cacaagtgtg gattgacttt      840
atggatgaaa gaaatttaag ctgggccaac tggtctctaa cgcataagga tgagtcatct      900
gcagcgttaa tgccaggtgc aaatccaact ggtggttgga cagaggctga actatctcca      960
```

```
tctggtacat ttgtgaggga aaaaataaga gaatcagcat ctgacaacaa tgatcccata      1020
```

<210> 134
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 134

```
Val Arg Ser Lys Lys Leu Trp Ile Ser Leu Leu Phe Ala Leu Thr Leu
1               5                   10                  15
Ile Phe Thr Met Ala Phe Ser Asn Met Ser Ala Gln Ala Asp Asp Tyr
            20                  25                  30
Ser Val Val Glu Glu His Gly Gln Leu Ser Ile Ser Asn Gly Glu Leu
            35                  40                  45
Val Asn Glu Arg Gly Glu Gln Val Gln Leu Lys Gly Met Ser Ser His


    50                  55                  60
Gly Leu Gln Trp Tyr Gly Gln Phe Val Asn Tyr Glu Ser Met Lys Trp
65                  70                  75                  80
Leu Arg Asp Asp Trp Gly Ile Thr Val Phe Arg Ala Ala Met Tyr Thr
            85                  90                  95
Ser Ser Gly Gly Tyr Ile Asp Asp Pro Ser Val Lys Glu Lys Val Lys
            100                 105                 110
Glu Thr Val Glu Ala Ala Ile Asp Leu Gly Ile Tyr Val Ile Ile Asp
            115                 120                 125
Trp His Ile Leu Ser Asp Asn Asp Pro Asn Ile Tyr Lys Glu Glu Ala
        130                 135                 140
Lys Asp Phe Phe Asp Glu Met Ser Glu Leu Tyr Gly Asp Tyr Pro Asn
145                 150                 155                 160
Val Ile Tyr Glu Ile Ala Asn Glu Pro Asn Gly Ser Asp Val Thr Trp
                165                 170                 175
Asp Asn Gln Ile Lys Pro Tyr Ala Glu Glu Val Ile Pro Val Ile Arg
            180                 185                 190
Asp Asn Asp Pro Asn Asn Ile Val Ile Val Gly Thr Gly Thr Trp Ser
        195                 200                 205
Gln Asp Val His His Ala Ala Asp Asn Gln Leu Ala Asp Pro Asn Val
    210                 215                 220
Met Tyr Ala Phe His Phe Tyr Ala Gly Thr His Gly Gln Asn Leu Arg
225                 230                 235                 240
Asp Gln Val Asp Tyr Ala Leu Asp Gln Gly Ala Ala Ile Phe Val Ser
                245                 250                 255
Glu Trp Gly Thr Ser Ala Ala Thr Gly Asp Gly Gly Val Phe Leu Asp
                260                 265                 270
Glu Ala Gln Val Trp Ile Asp Phe Met Asp Glu Arg Asn Leu Ser Trp
            275                 280                 285
Ala Asn Trp Ser Leu Thr His Lys Asp Glu Ser Ser Ala Ala Leu Met
    290                 295                 300
Pro Gly Ala Asn Pro Thr Gly Gly Trp Thr Glu Ala Glu Leu Ser Pro
305                 310                 315                 320
Ser Gly Thr Phe Val Arg Glu Lys Ile Arg Glu Ser Ala Ser Asp Asn
                325                 330                 335
Asn Asp Pro Ile
```

```
<210>  135
<211>  30
<212>  PRT
<213>  Cellulomonas strain 69B4
```

```
<400>  135
```

```
Met Arg Ser Lys Lys Arg Thr Val Thr Arg Ala Leu Ala Val Ala Thr
1               5                   10                  15
Ala Ala Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala
            20                  25                  30
```

```
<210>  136
<211>  30
<212>  PRT
<213>  Cellulomonas strain 69B4
```

```
<400>  136
```

```
Met Arg Ser Lys Lys Leu Trp Ile Ser Leu Leu Leu Ala Val Ala Thr
1               5                   10                  15
Ala Ala Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala
            20                  25                  30
```

```
<210>  137
<211>  40
<212>  DNA
<213>  Artificial Sequence
```

```
<220>
<223>  primer
```

```
<400>  137
ctagctaggt accatgacac cacgaactgt cacaagagct                          40
```

```
<210>  138
<211>  40
<212>  DNA
<213>  Artificial Sequence
```

```
<220>
<223>  primer
```

```
<400>  138
gtgtgcaagc tttcagggga gggtgagtcc cattgtgtaa                          40
```

```
<210>  139
<211>  40
<212>  DNA
<213>  Artificial Sequence
```

```
<220>
<223>  primer
```

```
<400>  139
```

```
ctagctaggt accatgacac cacgaactgt cacaagagct                              40

<210>  140
<211>  37
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  140
gtgtgcaagc tttcaagggg aacttccaga gtcagtc                                 37

<210>  141
<211>  53
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  141
tcatgcaggg taccatgaga agcaagaagc gaactgtcac aagagctctg gct              53

<210>  142
<211>  40
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  142
gtgtgcaagc tttcagggga gggtgagtcc cattgtgtaa                              40

<210>  143
<211>  53
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  143
tcatgcaggg taccatgaga agcaagaagc gaactgtcac aagagctctg gct              53

<210>  144
<211>  37
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  144
gtgtgcaagc tttcaagggg aacttccaga gtcagtc                                 37·
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```
<210>   145
<211>   74
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   145
tcatgcaggg taccatgaga agcaagaagt tgtggatcag tttgctgctg gctgtggcaa      60
cagcagctgc taca                                                       74

<210>   146
<211>   40
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   146
gtgtgcaagc tttcagggga gggtgagtcc cattgtgtaa                            40



<210>   147
<211>   74  .
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   147
tcatgcaggg taccatgaga agcaagaagt tgtggatcag tttgctgctg gctgtggcaa      60
cagcagctgc taca                                                       74

<210>   148
<211>   37
<212>   DNA

<213>   Artificial Sequence

<220>
<223>   primer

<400>   148
gtgtgcaagc tttcaagggg aacttccaga gtcagtc                               37

<210>   149
<211>   38
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer
```

<400> 149
ccataccgga tccaaacgaa ccggctcctc caggatct   38

<210> 150
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 150
ctcgagttaa gcttttaagg ggaacttcca gagtcagtc   39

<210> 151
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 151
tgagctgcta gcaaaaggag agggtaaaga atgacaccac gaactgtc   48

<210> 152
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 152
cgtacatccc gggtcagggg agggtgagtc ccattg   36

<210> 153
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 153
tgagctgcta gcaaaaggag agggtaaaga atgacaccac gaactgtc   48

<210> 154
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 154

```
catgcatccc gggttaaggg gaacttccag agtcagtc                           38


<210>  155
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  155
tgagctgcta gcaaaaggag agggtaaaga atgagaagca agaag                   45

<210>  156
<211>  36
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  156
cgtacatccc gggtcagggg agggtgagtc ccattg                             36

<210>  157
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  157
tgagctgcta gcaaaaggag agggtaaaga atgagaagca agaag                   45

<210>  158
<211>  38



<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  158
catgcatccc gggttaaggg gaacttccag agtcagtc                           38

<210>  159
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  159
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```
tgagctgcta gcaaaaggag agggtaaaga atgagaagca agaag                45


<210>  160
<211>  36
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  160
cgtacatccc gggtcagggg agggtgagtc ccattg                          36



<210>  161
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  161
tgagctgcta gcaaaaggag agggtaaaga atgagaagca agaag                45

<210>  162
<211>  38
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  162
catgcatccc gggttaaggg gaacttccag agtcagtc                        38

<210>  163
<211>  40
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  163
tgcagtctgc tagcaaaagg agagggtaaa gagtgagaag                      40

<210>  164
<211>  38
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  164
```

```
catgcatccc gggttaaggg gaacttccag agtcagtc                              38


<210>  165
<211>  50
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  165
ttatgcgagg ctagcaaaag gagagggtaa agagtgagaa gcaaaaaacg                 50


<210>  166
<211>  42
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  166
taaagagtga gaagcaaaaa acgcacagtc acgcgggccc tg                         42


<210>  167
<211>  35
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  167
gtcctctgtt aacttacggg ctgctgcccg agtcc                                 35


<210>  168
<211>  41
<212>  DNA

<213>  Artificial Sequence

<220>
<223>  primer

<400>  168
gcaacatgtc tgcgcaggct aacgaaccgg ctcctccagg a                          41


<210>  169
<211>  35
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  169
gacatgacat aagcttaagg ggaacttcca gagtc                                 35
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<210> 170
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 170
gagccgaatt catatacctg ccgtt   25

<210> 171
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 171
tcctggagga gccggttcgt tagcctgcgc agacatgttg c   41

<210> 172
<211> 5713
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 172
catcacatat acctgccgtt cactattatt tagtgaaatg agatattatg atattttctg   60
aattgtgatt aaaaaggcaa ctttatgccc atgcaacaga aactataaaa aatacagaga   120
atgaaaagaa acagatagat ttttttagttc tttaggcccg tagtctgcaa atccttttat   180
gattttctat caaacaaaag aggaaaatag accagttgca atccaaacga gagtctaata   240
gaatgaggtc acagaatagt ctttttaagta agtctactct gaattttttt aaaaggagag   300
ggtaaagagt gagaagcaaa aaattgtgga tcagcttgtt gtttgcgtta acgttaatct   360
ttacgatggc gttcagcaac atgtctgcgc aggctaacga accggctcct ccaggatctg   420
catcagcccc tccacgatta gctgaaaaac ttgaccctga cttacttgaa gcaatggaac   480
gcgatctggg gttagatgca gaggaagcag ctgcaacgtt agcttttcag catgacgcag   540
ctgaaacggg agaggctctt gctgaggaac tcgacgaaga tttcgcgggc acgtgggttg   600
aagatgatgt gctgtatgtt gcaaccactg atgaagatgc tgttgaagaa gtcgaaggcg   660
aaggagcaac tgctgtgact gttgagcatt ctcttgctga tttagaggcg tggaagacgg   720
tttttggatgc tgcgctggag ggtcatgatg atgtgcctac gtggtacgtc gacgtgccta   780
cgaattcggt agtcgttgct gtaaaggcag gagcgcagga tgtagctgca ggacttgtgg   840
aaggcgctga tgtgccatca gatgcggtca cttttgtaga aacggacgaa acgcctagaa   900
cgatgttcga cgtaattgga ggcaacgcat atactattgg cggccggtct agatgttcta   960
tcggattcgc agtaaacggt ggcttcatta ctgccggtca ctgcggaaga acaggagcca   1020
ctactgccaa tccgactggc acatttgcag gtagctcgtt ccgggaaat gattatgcat   1080
tcgtccgaac aggggcagga gtaaatttgc ttgcccaagt caataactac tcgggcggca   1140
gagtccaagt agcaggacat acggccgcac cagttggatc tgctgtatgc cgctcaggta   1200
gcactacagg ttggcattgc ggaactatca cggcgctgaa ttcgtctgtc acgtatccag   1260
agggaacagt ccgaggactt atccgcacga cggtttgtgc cgaaccaggt gatagcggag   1320
gtagcctttt agcgggaaat caagcccaag gtgtcacgtc aggtggttct ggaaattgtc   1380
ggacgggggg aacaacattc tttcaaccag tcaacccgat tttgcaggct tacggcctga   1440
gaatgattac gactgactct ggaagttccc cttaagctta aaaaaccggc cttggccccg   1500

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ccggttttttt attatttttc ttcctccgca tgttcaatcc gctccataat cgacggatgg    1560
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<210>   173
<211>   33
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   synthetic

<400>   173

Met Lys Lys Arg Thr Val Thr Arg Ala Leu Ala Val Ala Thr Ala Ala
1               5                   10                  15
Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala Asn Glu Pro Ala
            20                  25                  30
Pro


<210>   174
<211>   36
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   synthetic

<400>   174

Met Lys Lys Pro Leu Gly Arg Thr Val Thr Arg Ala Leu Ala Val Ala
1               5                   10                  15
Thr Ala Ala Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala Asn
            20                  25                  30
Glu Pro Ala Pro
        35

<210>   175
<211>   32
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   synthetic
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<400> 175

Met Lys Lys Pro Leu Gly Lys Ile Val Ala Ser Thr Ala Leu Leu Ile
1   5   10   15
Ser Val Ala Phe Ser Ser Ser Ile Ala Ser Ala Asn Glu Pro Ala Pro
            20   25   30

<210> 176
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 176
agggaaccga atgaagaaac gaactgtcac aagagctctg   40

<210> 177
<211> 40
<212> DNA
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<220>
<223> primer

<400> 177
cagagctctt gtgacagttc gtttcttcat tcggttccct   40

<210> 178
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 178
aatgaagaaa ccgttggggc gaactgtcac aagagctctg   40

<210> 179
<211> 40
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<220>
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<400> 179
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<400> 180
agttcatcga tcgcatcggc taacgaaccg gctcctccag ga   42

<210> 181
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<212> DNA
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<220>

<400> 181
tcctggagga gccggttcgt tagccgatgc gatcgatgaa ct   42

<210> 182
<211> 34
<212> DNA
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<220>

<400> 182
tcagggggat cctagattct gttaacttaa cgtt   34

<210> 183
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<212> DNA
<213> Artificial Sequence

<220>

<400> 183
gtgctgtttt atcctttacc ttgtctcc   28

<210> 184
<211> 29
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<400> 184
agttaagcaa tcagatcttc ttcaggtta   29

<210> 185
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<212> DNA
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<400> 185
cattgaaagg ggaggagaat catgagaagc aagaagcgaa ctgtcac   47

<210> 186
<211> 47
<212> DNA
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<220>
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<400> 186
gtgacagttc gcttcttgct tctcatgatt ctcctcccct ttcaatg   47

<210> 187

<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 187
ctttaccttg tctccaagct taaaataaaa aaacgg   36

<210> 188
<211> 28
<212> DNA
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<220>
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<400> 188
gcgcaggatg tagcagctgg acttgtgg   28

<210> 189
<211> 28
<212> DNA
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<220>
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<400> 189
ccacaagtcc agctgctaca tcctgcgc   28

<210> 190
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<212> DNA
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<220>
<223> primer

<400> 190

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gcctcattct gcagcttcag caaacgaacc ggctcctcca gg                           42


<210>  191
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<220>


<223>  primer

<400>  191
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<210>  192
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<400>  192
atcctactcg aggcttttct tttggaagaa aatataggg                               39


<210>  193
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<212>  DNA
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<220>
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<400>  193
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<210>  194
<211>  136
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  194
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tcggaatatt tatacaatat catatgtttc acattgaaag gggaggagaa tcatgaaaca        120
acaaaaacgg ctttac                                                       136


<210>  195
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<212>  DNA
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<220>
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<400> 195
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<210> 196
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
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<400> 196
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tcggaatatt tatacaatat catatgtttc acattgaaag gggaggagaa tcatgacacc   120
acgaactgtc acaag   135

<210> 197
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<212> DNA
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<220>
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<400> 197
attagtctcg aggatcgacc ggaccgcaac ctcc   34

<210> 198
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<212> DNA
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<220>
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<400> 198
cgatggcatt cagcgattcc gcttctgcta acgaaccggc tcctccagga tctgc   55

<210> 199
<211> 55
<212> DNA
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<220>
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<400> 199

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<210> 200
<211> 45
<212> DNA
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<220>
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<400> 200
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<210> 201
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<220>
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<400> 201
ggcgcgcctt aggggagggt gagccccatg gtgtaggcac cg   42

<210> 202
<211> 45
<212> DNA
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<220>
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<400> 202
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<210> 203
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<212> DNA
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<220>
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<400> 203
ggcgcgcctt acgggctgct gcccgagtcc gtggtgatca   40

<210> 204
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<213> Artificial Sequence

<220>
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<400> 204
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<210> 205
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<212> DNA
<213> Artificial Sequence

<220>
<223> primer

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<210>  206
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<213>  Artificial Sequence

<220>
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<400>  206
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<210>  207
<211>  30
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<220>
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<400>  209
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<220>
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<400> 211
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ggatct   66

<210> 212
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 212
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<210> 213
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 213
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ctcttggctg ggggtatggc agcacaagct   90

<210> 214
<211> 389
<212> PRT
<213> Cellulomonas strain 69B4

<400> 214

Met Arg Ser Lys Lys Arg Thr Val Thr Arg Ala Leu Ala Val Ala Thr
1   5   10   15
Ala Ala Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala Asn Glu
                20   25   30
Pro Ala Pro Pro Gly Ser Ala Ser Ala Pro Pro Arg Leu Ala Glu Lys
        35   40   45
Leu Asp Pro Asp Leu Leu Glu Ala Met Glu Arg Asp Leu Gly Leu Asp
    50   55   60
Ala Glu Glu Ala Ala Ala Thr Leu Ala Phe Gln His Asp Ala Ala Glu
65   70   75   80
Thr Gly Glu Ala Leu Ala Glu Glu Leu Asp Glu Asp Phe Ala Gly Thr

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                    85                    90                    95
Trp Val Glu Asp Asp Val Leu Tyr Val Ala Thr Thr Asp Glu Asp Ala
                100                   105                   110
Val Glu Glu Val Glu Gly Glu Gly Ala Thr Ala Val Thr Val Glu His
        115                   120                   125
Ser Leu Ala Asp Leu Glu Ala Trp Lys Thr Val Leu Asp Ala Ala Leu
    130                   135                   140
Glu Gly His Asp Asp Val Pro Thr Trp Tyr Val Asp Val Pro Thr Asn
145                   150                   155                   160
Ser Val Val Val Ala Val Lys Ala Gly Ala Gln Asp Val Ala Ala Gly
                165                   170                   175
Leu Val Glu Gly Ala Asp Val Pro Ser Asp Ala Val Thr Phe Val Glu
                180                   185                   190
Thr Asp Glu Thr Pro Arg Thr Met Phe Asp Val Ile Gly Gly Asn Ala
            195                   200                   205
Tyr Thr Ile Gly Gly Arg Ser Arg Cys Ser Ile Gly Phe Ala Val Asn
    210                   ·215                   220
Gly Gly Phe Ile Thr Ala Gly His Cys Gly Arg Thr Gly Ala Thr Thr
225                   230                   235                   240
Ala Asn Pro Thr Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp
                245                   250                   255
Tyr Ala Phe Val Arg Thr Gly Ala Gly Val Asn Leu Leu Ala Gln Val
                260                   265                   270
Asn Asn Tyr Ser Gly Gly Arg Val Gln Val Ala Gly His Thr Ala Ala
        275                   280                   285
Pro Val Gly Ser Ala Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His
    290                   ᴸ      295                   300
Cys Gly Thr Ile Thr Ala Leu Asn Ser Ser Val Thr Tyr Pro Glu Gly
305                   310                   315                   320
Thr Val Arg Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro Gly Asp
                325                   330                   335
Ser Gly Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val Thr Ser
            340                   345                   350
Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe Gln Pro
        355                   360                   365
Val Asn Pro Ile Leu Gln Ala Tyr Gly Leu Arg Met Ile Thr Thr Asp
    370                   375                   380
Ser Gly Ser Ser Pro
385


<210>  215
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<212>  DNA
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<220>
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<400>  215
gcaatcagat cttccttcag gttatgacc                                     29

<210>  216
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<223> primer

<400> 216
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<210> 217
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<220>
<223> primer

<220>
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<222> (19)..(20)
<223> n is a, c, g, or t

<400> 217
gaaacgccta gaacgatgnn sgacgtaatt ggaggcaac   39

<210> 218
<211> 39
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<220>
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<400> 218
acgcctagaa cgatgttcnn sgtaattgga ggcaacgca   39

<210> 219
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<210> 220
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<220>
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<400>   221
acgatgttcg acgtaattnn sggcaacgca tatactatt                              39

<210>   222
<211>   39
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<400>   222
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<210>   223
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<223>   n is a, c, g, or t
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<210>  224
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<400>  224
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<210>  225
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<400>  225
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<210>  226
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<400>  226
attggaggca acgcatatnn sattggcggc cggtctaga                              39


<210>  227
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<223> primer

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<400> 227
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<210> 228
<211> 39
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<220>
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<220>
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<222> (19)..(20)
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<400> 228
ggcaacgcat atactattnn sggccggtct agatgttct   39

<210> 229
<211> 39
<212> DNA
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<220>
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<211>  39
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<220>
<221>  misc_feature
<222>  (20)..(21)
<223>  n is a, c, g, or t

<400>  588
aggggaactt ccagagtcsn ncgtaatcat tctcaggcc                                    39

<210>  589
<211>  39
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<220>
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<222>  (20)..(21)
<223>  n is a, c, g, or t

<400>  589
ttaaggggaa cttccagasn nagtcgtaat cattctcag                                    39

<210>  590
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<211> 39

<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<220>
<221> misc_feature
<222> (20)..(21)
<223> n is a, c, g, or t

<400> 590
gggttaaggg gaacttccsn ngtcagtcgt aatcattct   39

<210> 591
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<220>
<221> misc_feature
<222> (20)..(21)
<223> n is a, c, g, or t

<400> 591
gttgggttaa ggggaactsn nagagtcagt cgtaatcat   39

<210> 592
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<212> DNA
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<220>
<223> primer

<220>
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<222> (20)..(21)
<223> n is a, c, g, or t

<400> 592
tctgttgggt taaggggasn ntccagagtc agtcgtaat   39

<210> 593

<211> 39
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<220>
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<223> n is a, c, g, or t

<400> 593
tcctctgttg ggttaaggsn nacttccaga gtcagtcgt   39

<210> 594
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<220>
<221> misc_feature
<222> (20)..(21)
<223> n is a, c, g, or t

<400> 594
ccgtcctctg ttgggttasn nggaacttcc agagtcagt   39

<210> 595
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 595
gcatatacta ttggcggcct gtctagatgt tctatcgga   39

<210> 596
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 596
actattggcg gccggtctca gtgttctatc ggattcgc   38

<210> 597
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 597
ctgccggtca ctgcggattt acaggagcca ctactgc   37

<210> 598
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
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<400> 598
atgattatgc attcgtctca acaggggcag gagtaaat   38

<210> 599
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 599
ataactactc gggcggcaca gtccaagtag caggacatac   40

<210> 600
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 600
atccagaggg aacagtcctg ggacttatcc gcacgac   37

<210> 601
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 601
cagtccgagg acttatccag acgacggttt gtgccgaac   39

<210> 602
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 602
gtggttctgg aaattgtcag acggggggaa caacattc   38

<210> 603
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 603
tgcaggctta cggcctgcag atgattacga ctgactc   37

<210> 604
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 604
ttggcggccg gtctagatca tctatcggat tcgcagta   38

<210> 605
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 605
tcattactgc cggtcactca ggaagaacag gagccact   38

<210> 606
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 606
cagttggatc tgctgtatct cgctcaggta gcactac   37

<210> 607
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 607
cactacaggt tggcattcag gaactatcac ggcgctg   37

<210> 608
<211> 38

<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 608
cttatccgca cgacggtttc agccgaacca ggtgatag   38

<210> 609
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 609
caggtggttc tggaaattca cggacggggg gaacaac   37

<210> 610
<211> 19
<212> DNA
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<220>
<223> primer

<400> 610
tgcctcacat ttgtgccac   19

<210> 611
<211> 19
<212> DNA
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<220>
<223> primer

<400> 611
caggatgtag ctgcaggac   19

<210> 612
<211> 19
<212> DNA
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<220>
<223> primer

<400> 612
ctcggttatg agttagttc   19

<210> 613
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
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<400> 613
cagagacaga cccccggagg taaccatggc acgatcattc tggaggacgc   50

<210> 614
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 614
gcgtcctcca gaatgatcgt gccatggtta cctccggggg tctgtctctg   50

<210> 615
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 615
atccgctcgc ggatccccat tgtcagctcg ggcccccacc gtcagaggtc acgag   55

<210> 616
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 616
gcagcctgaa ctagttgcga tcctctagag atcgaacttc at   42

<210> 617
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 617
agaccgacga gacccgcgg accatggtcg acgtcatcgg cggcaacgcg tactac   56

<210> 618
<211> 56
<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<400> 618
tcagccgatc cgctcgcgga tccccattgt cagcccagga cgagacgcag accgta   56

<210> 619
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 619
gtagtacgcg ttgccgccga tgacgtcgac catggtccgc ggggtctcgt cggtct   56

<210> 620
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 620
gcagcctgaa ctagttgcga tcctctagag atcgaacttc atgttcga   48

<210> 621
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 621
accgacgaga ccccgcggac catgcacggc gacgtgcgcg gcggcgaccg cta   53

<210> 622
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 622
tagcggtcgc cgccgcgcac gtcgccgtgc atggtccgcg gggtctcgtc ggt   53

<210> 623
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 623
tcagccgatc cgctcgcgga tccccattgt cagcgagccc gacgagcgcg ctgcccgac   59

<210> 624
<211> 184
<212> PRT
<213> Cellulomonas strain 69B4

<400> 624

Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr Ile Gly Gly Arg Ser Arg
1   5   10   15
Cys Ser Ile Gly Phe Ala Val Asn Gly Gly Phe Ile Thr Ala Gly His
            20   25   30
Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala
            35   40   45
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala
            50   55   60
Gly Val Asn Leu Leu Ala Gln Val Asn Asn Tyr Ser Gly Gly Arg Val
65   70   75   80
Gln Val Ala Gly His Thr Ala Ala Pro Val Gly Ser Ala Val Cys Arg
            85   90   95
Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Thr Ala Leu Asn
            100   105   110
Ser Ser Val Thr Tyr Pro Glu Gly Thr Val Arg Gly Leu Ile Arg Thr
            115   120   125
Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly
            130   135   140
Asn Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr
145   150   155   160
Gly Gly Thr Thr Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr
                165   170   175
Gly Leu Arg Met Ile Thr Thr Asp
            180

<210> 625
<211> 187
<212> PRT
<213> Streptomyces griseus

<400> 625

Val Leu Gly Gly Gly Ala Ile Tyr Gly Gly Gly Ser Arg Cys Ser Ala
1   5   10   15
Ala Phe Asn Val Thr Lys Gly Gly Ala Arg Tyr Phe Val Thr Ala Gly
            20   25   30
His Cys Thr Asn Ile Ser Ala Asn Trp Ser Ala Ser Ser Gly Gly Ser
            35   40   45
Val Val Gly Val Arg Glu Gly Thr Ser Phe Pro Thr Asn Asp Tyr Gly
            50   55   60
Ile Val Arg Tyr Thr Asp Gly Ser Ser Pro Ala Gly Thr Val Asp Leu
65   70   75   80
Tyr Asn Gly Ser Thr Gln Asp Ile Ser Ser Ala Ala Asn Ala Val Val
            85   90   95
Gly Gln Ala Ile Lys Lys Ser Gly Ser Thr Thr Lys Val Thr Ser Gly
            100   105   110
Thr Val Thr Ala Val Asn Val Thr Val Asn Tyr Gly Asp Gly Pro Val

```
                115                       120                       125
Tyr Asn Met Val Arg Thr Thr Ala Cys Ser Ala Gly Gly Asp Ser Gly
        130                       135                       140
Gly Ala His Phe Ala Gly Ser Val Ala Leu Gly Ile His Ser Gly Ser
145                       150                       155                       160
Ser Gly Cys Ser Gly Thr Ala Gly Ser Ala Ile His Gln Pro Val Thr
                165                       170                       175
Glu Ala Leu Ser Ala Tyr Gly Val Thr Val Tyr
            180                       185


<210>  626
<211>  185
<212>  PRT
<213>  Streptomyces griseus


<400>  626

Ile Ser Gly Gly Asp Ala Ile Tyr Ser Ser Thr Gly Arg Cys Ser Leu
1                   5                   10                  15
Gly Phe Asn Val Arg Ser Gly Ser Thr Tyr Tyr Phe Leu Thr Ala Gly
                20                      25                      30
His Cys Thr Asp Gly Ala Thr Thr Trp Trp Ala Asn Ser Ala Arg Thr
            35                      40                      45
Thr Val Leu Gly Thr Thr Ser Gly Ser Ser Phe Pro Asn Asn Asp Tyr
        50                      55                      60
Gly Ile Val Arg Tyr Thr Asn Thr Thr Ile Pro Lys Asp Gly Thr Val
65                      70                      75                      80
Gly Gly Gln Asp Ile Thr Ser Ala Ala Asn Ala Thr Val Gly Met Ala
                85                      90                      95
Val Thr Arg Arg Gly Ser Thr Thr Gly Thr His Ser Gly Ser Val Thr
                100                     105                     110
Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Gly Asp Val Val Tyr Gly
            115                     120                     125


Met Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Pro
        130                     135                     140
Leu Tyr Ser Gly Thr Arg Ala Ile Gly Leu Thr Ser Gly Gly Ser Gly
145                     150                     155                     160
Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val Thr Glu Ala
                165                     170                     175
Leu Val Ala Tyr Gly Val Ser Val Tyr
            180                     185


<210>  627
<211>  198
<212>  PRT

<213>  Lysobacter enzymogenes


<400>  627

Ala Asn Ile Val Gly Gly Ile Glu Tyr Ser Ile Asn Asn Ala Ser Leu
1                   5                   10                  15
Cys Ser Val Gly Phe Ser Val Thr Arg Gly Ala Thr Lys Gly Phe Val
                20                      25                      30
Thr Ala Gly His Cys Gly Thr Val Asn Ala Thr Ala Arg Ile Gly Gly
```

```
              35                    40                    45
Ala Val Val Gly Thr Phe Ala Ala Arg Val Phe Pro Gly Asn Asp Arg
    50                    55                    60
Ala Trp Val Ser Leu Thr Ser Ala Gln Thr Leu Leu Pro Arg Val Ala
65                    70                    75                    80
Asn Gly Ser Ser Phe Val Thr Val Arg Gly Ser Thr Glu Ala Ala Val
                  85                    90                    95
Gly Ala Ala Val Cys Arg Ser Gly Arg Thr Thr Gly Tyr Gln Cys Gly
              100                   105                   110
Thr Ile Thr Ala Lys Asn Val Thr Ala Asn Tyr Ala Glu Gly Ala Val
              115                   120                   125
Arg Gly Leu Thr Gln Gly Asn Ala Cys Met Gly Arg Gly Asp Ser Gly
          130                   135                   140
Gly Ser Trp Ile Thr Ser Ala Gly Gln Ala Gln Gly Val Met Ser Gly
145                   150                   155                   160
Gly Asn Val Gln Ser Asn Gly Asn Asn Cys Gly Ile Pro Ala Ser Gln
                  165                   170                   175
Arg Ser Ser Leu Phe Glu Arg Leu Gln Pro Ile Leu Ser Gln Tyr Gly
              180                   185                   190
Leu Ser Leu Val Thr Gly
          195


<210>   628
<211>   191
<212>   PRT
<213>   Streptomyces fradiae


<400>   628

Ile Ala Gly Gly Glu Ala Ile Tyr Ala Ala Gly Gly Gly Arg Cys Ser
1               5                     10                    15
Leu Gly Phe Asn Val Arg Ser Ser Ser Gly Ala Thr Tyr Ala Leu Thr
              20                    25                    30
Ala Gly His Cys Thr Glu Ile Ala Ser Thr Trp Tyr Thr Asn Ser Gly
          35                    40                    45
Gln Thr Ser Leu Leu Gly Thr Arg Ala Gly Thr Ser Phe Pro Gly Asn
    50                    55                    60
Asp Tyr Gly Leu Ile Arg His Ser Asn Ala Ser Ala Ala Asp Gly Arg
65                    70                    75                    80
Val Tyr Leu Tyr Asn Gly Ser Tyr Arg Asp Ile Thr Gly Ala Gly Asn
                  85                    90                    95
Ala Tyr Val Gly Gln Thr Val Gln Arg Ser Gly Ser Thr Thr Gly Leu
              100                   105                   110
His Ser Gly Arg Val Thr Gly Leu Asn Ala Thr Val Asn Tyr Gly Gly
          115                   120                   125
Gly Asp Ile Val Ser Gly Leu Ile Gln Thr Asn Val Cys Ala Glu Pro
      130                   135                   140
Gly Asp Ser Gly Gly Ala Leu Phe Ala Gly Ser Thr Ala Leu Gly Leu
145                   150                   155                   160
Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe
                  165                   170                   175
Gln Pro Val Thr Glu Ala Leu Ser Ala Tyr Gly Val Ser Ile Leu
              180                   185                   190


<210>   629
<211>   181
<212>   PRT
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<210> Streptomyces griseus

<400> 629

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Ile Ala Gly Gly Glu Ala Ile Thr Thr Gly Gly Ser Arg Cys Ser Leu
1               5                   10                  15
Gly Phe Asn Val Ser Val Asn Gly Val Ala His Ala Leu Thr Ala Gly
            20                  25                  30
His Cys Thr Asn Ile Ser Ala Ser Trp Ser Ile Gly Thr Arg Thr Gly
            35                  40                  45
Thr Ser Phe Pro Asn Asn Asp Tyr Gly Ile Ile Arg His Ser Asn Pro
        50                  55                  60
Ala Ala Ala Asp Gly Arg Val Tyr Leu Tyr Asn Gly Ser Tyr Gln Asp
65                  70                  75                  80
Ile Thr Thr Ala Gly Asn Ala Phe Val Gly Gln Ala Val Gln Arg Ser
                85                  90                  95
Gly Ser Thr Thr Gly Leu Arg Ser Gly Ser Val Thr Gly Leu Asn Ala
            100                 105                 110
Thr Val Asn Tyr Gly Ser Ser Gly Ile Val Tyr Gly Met Ile Gln Thr
            115                 120                 125
Asn Val Cys Ala Gln Pro Gly Asp Ser Gly Gly Ser Leu Phe Ala Gly
    130                 135                 140
Ser Thr Ala Leu Gly Leu Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr
145                 150                 155                 160
Gly Gly Thr Thr Phe Tyr Gln Pro Val Thr Glu Ala Leu Ser Ala Tyr
                165                 170                 175
Gly Ala Thr Val Leu
            180
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<210> 630
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 630

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Pro Arg Thr Met Phe Asp
1               5
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<210> 631
<211> 10
<212> PRT
<213> Cellulomonas strain 69B4

<400> 631

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Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr
1               5                   10
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<210> 632
<211> 9
<212> PRT
<213> Cellulomonas strain 69B4

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<400>  632

Thr Ala Asn Pro Thr Gly Thr Phe Ala
1               5

<210>  633
<211>  12
<212>  PRT
<213>  Cellulomonas strain 69B4

<400>  633

Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala
1               5                   10

<210>  634
<211>  14
<212>  PRT
<213>  Cellulomonas strain 69B4

<400>  634

Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val
1               5                   10

<210>  635
<211>  10
<212>  PRT
<213>  Cellulomonas strain 69B4

<400>  635

Arg Thr Gly Ala Gly Val Asn Leu Leu Ala
1               5                   10

<210>  636
<211>  9
<212>  PRT
<213>  Cellulomonas strain 69B4

<400>  636

Phe Phe Gln Pro Val Asn Pro Ile Leu
1               5

<210>  637

<211>  11
<212>  PRT
<213>  Cellulomonas strain 69B4

<400>  637

Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala
1               5                   10
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<210> 638
<211> 13
<212> PRT
<213> Cellulomonas strain 69B4

<400> 638

Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr Gly
1   5   10

<210> 639
<211> 255
<212> PRT
<213> Streptogrisin C

<400> 639

Ala Asp Ile Arg Gly Gly Asp Ala Tyr Tyr Met Asn Gly Ser Gly Arg
1   5   10   15
Cys Ser Val Gly Phe Ser Val Thr Arg Gly Thr Gln Asn Gly Phe Ala
            20   25   30
Thr Ala Gly His Cys Gly Arg Val Gly Thr Thr Thr Asn Gly Val Asn
        35   40   45
Gln Gln Ala Gln Gly Thr Phe Gln Gly Ser Thr Phe Pro Gly Arg Asp
    50   55   60
Ile Ala Trp Val Ala Thr Asn Ala Asn Trp Thr Pro Arg Pro Leu Val
65   70   75   80
Asn Gly Tyr Gly Arg Gly Asp Val Thr Val Ala Gly Ser Thr Ala Ser
            85   90   95
Val Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His
            100   105   110
Cys Gly Thr Ile Gln Gln Leu Asn Thr Ser Val Thr Tyr Pro Glu Gly
            115   120   125
Thr Ile Ser Gly Val Thr Arg Thr Ser Val Cys Ala Glu Pro Gly Asp
        130   135   140
Ser Gly Gly Ser Tyr Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser
145   150   155   160
Gly Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Tyr Phe Gln Pro
                165   170   175
Ile Asn Pro Leu Leu Gln Ala Tyr Gly Leu Thr Leu Val Thr Ser Gly
            180   185   190
Gly Gly Thr Pro Thr Asp Pro Pro Thr Thr Pro Pro Thr Asp Ser Pro
        195   200   205
Gly Gly Thr Trp Ala Val Gly Thr Ala Tyr Ala Ala Gly Ala Thr Val
    210   215   220
Thr Tyr Gly Gly Ala Thr Tyr Arg Cys Leu Gln Ala His Thr Ala Gln
225   230   235   240
Pro Gly Trp Thr Pro Ala Asp Val Pro Ala Leu Trp Gln Arg Val
                245   250   255

<210> 640
<211> 185
<212> PRT
<213> Streptogrisin B

<400> 640

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Ile Ser Gly Gly Asp Ala Ile Tyr Ser Ser Thr Gly Arg Cys Ser Leu
1               5                   10                  15
Gly Phe Asn Val Arg Ser Gly Ser Thr Tyr Tyr Phe Leu Thr Ala Gly


                20                  25                  30
His Cys Thr Asp Gly Ala Thr Thr Trp Trp Ala Asn Ser Ala Arg Thr
        35                  40                  45
Thr Val Leu Gly Thr Thr Ser Gly Ser Ser Phe Pro Asn Asn Asp Tyr
    50                  55                  60
Gly Ile Val Arg Tyr Thr Asn Thr Thr Ile Pro Lys Asp Gly Thr Val
65                  70                  75                      80
Gly Gly Gln Asp Ile Thr Ser Ala Ala Asn Ala Thr Val Gly Met Ala
                85                  90                  95
Val Thr Arg Arg Gly Ser Thr Thr Gly Thr His Ser Gly Ser Val Thr
            100                 105                 110
Ala Leu Asn Ala Thr Val Asn Tyr Gly Gly Gly Asp Val Val Tyr Gly
        115                 120                 125
Met Ile Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Pro
    130                 135                 140
Leu Tyr Ser Gly Thr Arg Ala Ile Gly Leu Thr Ser Gly Gly Ser Gly
145                 150                 155                 160
Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val Thr Glu Ala
            165                 170                 175
Leu Ser Ala Tyr Gly Val Ser Val Tyr
            180                 185

<210>   641
<211>   181
<212>   PRT
<213>   Streptogrisin A

<400>   641

Ile Ala Gly Gly Glu Ala Ile Thr Thr Gly Gly Ser Arg Cys Ser Leu
1               5                   10                  15
Gly Phe Asn Val Ser Val Asn Gly Val Ala His Ala Leu Thr Ala Gly
                20                  25                  30
His Cys Thr Asn Ile Ser Ala Ser Trp Ser Ile Gly Thr Arg Thr Gly
        35                  40                  45
Thr Ser Phe Pro Asn Asn Asp Tyr Gly Ile Ile Arg His Ser Asn Pro
    50                  55                  60
Ala Ala Ala Asp Gly Arg Val Tyr Leu Tyr Asn Gly Ser Tyr Gln Asp
65                  70                  75                      80
Ile Thr Thr Ala Gly Asn Ala Phe Val Gly Gln Ala Val Gln Arg Ser
                85                  90                  95
Gly Ser Thr Thr Gly Leu Arg Ser Gly Ser Val Thr Gly Leu Asn Ala
            100                 105                 110
Thr Val Asn Tyr Gly Ser Ser Gly Ile Val Tyr Gly Met Ile Gln Thr
        115                 120                 125
Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Phe Ala Gly
    130                 135                 140
Ser Thr Ala Leu Gly Leu Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr
145                 150                 155                 160
Gly Gly Thr Thr Phe Tyr Gln Pro Val Thr Glu Ala Leu Ser Ala Tyr
            165                 170                 175
Gly Ala Thr Val Leu
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<210> 642
<211> 188
<212> PRT
<213> Streptogrisin D

<400> 642

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Ile Ala Gly Gly Asp Ala Ile Trp Gly Ser Gly Ser Arg Cys Ser Leu
1               5                   10                  15
Gly Phe Asn Val Val Lys Gly Gly Glu Pro Tyr Phe Leu Thr Ala Gly
            20                  25                  30
His Cys Thr Glu Ser Val Thr Ser Trp Ser Asp Thr Gln Gly Gly Ser
            35                  40                  45
Glu Ile Gly Ala Asn Glu Gly Ser Ser Phe Pro Glu Asn Asp Tyr Gly
    50                  55                  60
Leu Val Lys Tyr Thr Ser Asp Thr Ala His Pro Ser Glu Val Asn Leu
65                  70                  75                  80
Tyr Asp Gly Ser Thr Gln Ala Ile Thr Gln Ala Gly Asp Ala Thr Val
                85                  90                  95
Gly Gln Ala Val Thr Arg Ser Gly Ser Thr Thr Gln Val His Asp Gly
                100                 105                 110
Glu Val Thr Ala Leu Asp Ala Thr Val Asn Tyr Gly Asn Gly Asp Ile
        115                 120                 125
Val Asn Gly Leu Ile Gln Thr Thr Val Cys Ala Glu Pro Gly Asp Ser
    130                 135                 140
Gly Gly Ala Leu Phe Ala Gly Asp Thr Ala Leu Gly Leu Thr Ser Gly
145                 150                 155                 160
Gly Ser Gly Asp Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln Pro Val
                165                 170                 175
Pro Glu Ala Leu Ala Ala Tyr Gly Ala Glu Ile Gly
                180                 185
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<210> 643
<211> 198
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<220>
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<222> (9)..(10)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (12)..(12)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (22)..(23)

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<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  VARIANT
<222>  (25)..(27)
<223>  Xaa can be any naturally occurring amino acid

<220>
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<222>  (37)..(38)
<223>  Xaa can be any naturally occurring amino acid

<220>
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<222>  (43)..(51)
<223>  Xaa can be any naturally occurring amino acid

<220>
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<222>  (55)..(56)
<223>  Xaa can be any naturally occurring amino acid

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<223>  Xaa can be any naturally occurring amino acid

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<223>  Xaa can be any naturally occurring amino acid

<220>
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<223>  Xaa can be any naturally occurring amino acid

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<223>  Xaa can be any naturally occurring amino acid

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<223>  Xaa can be any naturally occurring amino acid

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<222>  (89)..(89)
<223>  Xaa can be any naturally occurring amino acid

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<223>  Xaa can be any naturally occurring amino acid
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<220>
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<222>  (95)..(95)
<223>  Xaa can be any naturally occurring amino acid

<220>
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<222>  (97)..(97)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  VARIANT
<222>  (100)..(100)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  VARIANT
<222>  (103)..(103)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  VARIANT
<222>  (111)..(111)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  VARIANT
<222>  (113)..(113)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  VARIANT
<222>  (127)..(127)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  VARIANT
<222>  (129)..(129)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  VARIANT
<222>  (132)..(132)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  VARIANT
<222>  (155)..(155)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  VARIANT
<222>  (179)..(179)
<223>  Xaa can be any naturally occurring amino acid

<220>
```

<221> VARIANT
<222> (191)..(198)
<223> Xaa can be any naturally occurring amino acid

<400> 643

```
Ile Ala Gly Gly Asp Ala Ile Tyr Xaa Xaa Gly Xaa Ser Arg Cys Ser
1               5                   10                  15
Leu Gly Phe Asn Val Xaa Xaa Gly Xaa Xaa Xaa Tyr Phe Leu Thr Ala
            20              25                  30
Gly His Cys Thr Xaa Xaa Gly Thr Thr Trp Xaa Xaa Xaa Xaa Xaa Xaa
        35              40                  45
Xaa Xaa Xaa Ile Gly Thr Xaa Xaa Gly Ser Ser Phe Pro Xaa Asn Asp
    50              55                  60
Tyr Gly Ile Val Arg Tyr Thr Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val
65              70                  75                  80
Asn Xaa Tyr Xaa Gly Xaa Xaa Gln Xaa Ile Thr Xaa Ala Gly Xaa Ala
        85                  90                  95
Xaa Val Gly Xaa Ala Val Xaa Arg Ser Gly Ser Thr Thr Gly Xaa His
        100                 105                 110
Xaa Gly Ser Val Thr Ala Leu Asn Ala Thr Val Asn Tyr Gly Xaa Gly
        115                 120                 125
Xaa Ile Val Xaa Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro Gly
    130             135                 140
Asp Ser Gly Gly Ser Leu Phe Ala Gly Ser Xaa Ala Leu Gly Leu Thr
145             150                 155                 160
Ser Gly Gly Ser Gly Asn Cys Ser Ser Gly Gly Thr Thr Phe Phe Gln
            165                 170                 175
Pro Val Xaa Glu Ala Leu Ser Ala Tyr Gly Leu Thr Val Ile Xaa Xaa
            180                 185                 190
Xaa Xaa Xaa Xaa Xaa Xaa
        195
```

<210> 644
<211> 513
<212> PRT
<213> Thermus aquaticus

<400> 644

```
Met Arg Lys Thr Tyr Trp Leu Met Ala Leu Phe Ala Val Leu Val Leu
1               5                   10                  15
Gly Gly Cys Gln Met Ala Ser Arg Ser Asp Pro Thr Pro Thr Leu Ala
            20              25                  30
Glu Ala Phe Trp Pro Lys Glu Ala Pro Val Tyr Gly Leu Asp Asp Pro
            35              40                  45
Glu Ala Ile Pro Gly Arg Tyr Ile Val Val Phe Lys Lys Gly Lys Gly
    50              55                  60
Gln Ser Leu Leu Gln Gly Gly Ile Thr Thr Leu Gln Ala Arg Leu Ala
65              70                  75                  80
Pro Gln Gly Val Val Val Thr Gln Ala Tyr Thr Gly Ala Leu Gln Gly
            85                  90                  95
Phe Ala Ala Glu Met Ala Pro Gln Ala Leu Glu Ala Phe Arg Gln Ser
            100                 105                 110
Pro Asp Val Glu Phe Ile Glu Ala Asp Lys Val Val Arg Ala Trp Ala
            115                 120                 125
Thr Gln Ser Pro Ala Pro Trp Gly Leu Asp Arg Ile Asp Gln Arg Asp
```

```
          130                     135                     140
Leu Pro Leu Ser Asn Ser Tyr Thr Tyr Thr Ala Thr Gly Arg Gly Val
145                     150                     155                     160
Asn Val Tyr Val Ile Asp Thr Gly Ile Arg Thr Thr His Arg Glu Phe
                165                     170                     175
Gly Gly Arg Ala Arg Val Gly Tyr Asp Ala Leu Gly Gly Asn Gly Gln
                180                     185                     190
Asp Cys Asn Gly His Gly Thr His Val Ala Gly Thr Ile Gly Gly Val
                195                     200                     205
Thr Tyr Gly Val Ala Lys Ala Val Asn Leu Tyr Ala Val Arg Val Leu
        210                     215                     220
Asp Cys Asn Gly Ser Gly Ser Thr Ser Gly Val Ile Ala Gly Val Asp
225                     230                     235                     240
Trp Val Thr Arg Asn His Arg Arg Pro Ala Val Ala Asn Met Ser Leu
                245                     250                     255
Gly Gly Gly Val Ser Thr Ala Leu Asp Asn Ala Val Lys Asn Ser Ile
                260                     265                     270
Ala Ala Gly Val Val Tyr Ala Val Ala Ala Gly Asn Asp Asn Ala Asn
                275                     280                     285
Ala Cys Asn Tyr Ser Pro Ala Arg Val Ala Glu Ala Leu Thr Val Gly
        290                     295                     300
Ala Thr Thr Ser Ser Asp Ala Arg Ala Ser Phe Ser Asn Tyr Gly Ser
305                     310                     315                     320
Cys Val Asp Leu Phe Ala Pro Gly Ala Ser Ile Pro Ser Ala Trp Tyr
                325                     330                     335
Thr Ser Asp Thr Ala Thr Gln Thr Leu Asn Gly Thr Ser Met Ala Thr
                340                     345                     350
Pro His Val Ala Gly Val Ala Ala Leu Tyr Leu Glu Gln Asn Pro Ser
                355                     360                     365
Ala Thr Pro Ala Ser Val Ala Ser Ala Ile Leu Asn Gly Ala Thr Thr
        370                     375                     380
Gly Arg Leu Ser Gly Ile Gly Ser Gly Ser Pro Asn Arg Leu Leu Tyr
385                     390                     395                     400
Ser Leu Leu Ser Ser Gly Ser Gly Ser Thr Ala Pro Cys Thr Ser Cys
                405                     410                     415
Ser Tyr Tyr Thr Gly Ser Leu Ser Gly Pro Gly Asp Tyr Asn Phe Gln
                420                     425                     430
Pro Asn Gly Thr Tyr Tyr Ser Pro Ala Gly Thr His Arg Ala Trp
                435                     440                     445
Leu Arg Gly Pro Ala Gly Thr Asp Phe Asp Leu Tyr Leu Trp Arg Trp
        450                     455                     460
Asp Gly Ser Arg Trp Leu Thr Val Gly Ser Ser Thr Gly Pro Thr Ser
465                     470                     475                     480
Glu Glu Ser Leu Ser Tyr Ser Gly Thr Ala Gly Tyr Tyr Leu Trp Arg
                485                     490                     495
Ile Tyr Ala Tyr Ser Gly Ser Gly Met Tyr Glu Phe Trp Leu Gln Arg
                500                     505                     510
Pro
```

```
Met Thr Pro Arg Thr Val Thr Arg Ala Leu Ala Val Ala Thr Ala Ala
1             5                   10              15
Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala Asn Glu Pro Ala
            20                  25                  30
Pro Pro Gly Ser Ala Ser Ala Pro Pro Arg Leu Ala Glu Lys Leu Asp
        35                  40                  45
Pro Asp Leu Leu Glu Ala Met Glu Arg Asp Leu Gly Leu Asp Ala Glu
    50                  55                  60
Glu Ala Ala Ala Thr Leu Ala Phe Gln His Asp Ala Ala Glu Thr Gly
65                  70                  75                  80
Glu Ala Leu Ala Glu Glu Leu Asp Glu Asp Phe Ala Gly Thr Trp Val
            85                  90                  95
Glu Asp Asp Val Leu Tyr Val Ala Thr Thr Asp Glu Asp Ala Val Glu
            100                 105                 110
Glu Val Glu Gly Glu Gly Ala Thr Ala Val Thr Val Glu His Ser Leu
        115                 120                 125
Ala Asp Leu Glu Ala Trp Lys Thr Val Leu Asp Ala Ala Leu Glu Gly
    130                 135                 140
His Asp Asp Val Pro Thr Trp Tyr Val Asp Val Pro Thr Asn Ser Val
145                 150                 155                 160
Val Val Ala Val Lys Ala Gly Ala Gln Asp Val Ala Ala Gly Leu Val
                165                 170                 175
Glu Gly Ala Asp Val Pro Ser Asp Ala Val Thr Phe Val Glu Thr Asp
            180                 185                 190
Glu Thr Pro Arg Thr Met Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr
            195                 200                 205
Ile Gly Gly Arg Ser Arg Cys Ser Ile Gly Phe Ala Val Asn Gly Gly
    210                 215                 220
Phe Ile Thr Ala Gly His Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn
225                 230                 235                 240
Pro Thr Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala
            245                 250                 255
Phe Val Arg Thr Gly Ala Gly Val Asn Leu Leu Ala Gln Val Asn Asn
            260                 265                 270
Tyr Ser Gly Gly Arg Val Gln Val Ala Gly His Thr Ala Ala Pro Val
    275                 280                 285
Gly Ser Ala Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly
    290                 295                 300
Thr Ile Thr Ala Leu Asn Ser Ser Val Thr Tyr Pro Glu Gly Thr Val
305                 310                 315                 320
Arg Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
            325                 330                 335
Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val Thr Ser Gly Gly
            340                 345                 350
Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe Gln Pro Val Asn
    355                 360                 365
Pro Ile Leu Gln Ala Tyr Gly Leu Arg Met Ile Thr Thr Asp Ser Gly
    370                 375                 380
Ser Ser Pro Ala Pro Ala Pro Thr Ser Cys Thr Gly Tyr Ala Arg Thr
385                 390                 395                 400
Phe Thr Gly Thr Leu Ala Ala Gly Arg Ala Ala Ala Gln Pro Asn Gly
            405                 410                 415
Ser Tyr Val Gln Val Asn Arg Ser Gly Thr His Ser Val Cys Leu Asn
            420                 425                 430
Gly Pro Ser Gly Ala Asp Phe Asp Leu Tyr Val Gln Arg Trp Asn Gly
    435                 440                 445
Ser Ser Trp Val Thr Val Ala Gln Ser Thr Ser Pro Gly Ser Asn Glu
```

```
       450                    455                    460
Thr Ile Thr Tyr Arg Gly Asn Ala Gly Tyr Tyr Arg Tyr Val Val Asn
465                    470                    475                    480
Ala Ala Ser Gly Ser Gly Ala Tyr Thr Met Gly Leu Thr Leu Pro
                   485                    490                    495
```

```
<210>  646
<211>  510
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  consensus sequence

<220>
<221>  VARIANT
<222>  (3)..(509)
<223>  Xaa can be any naturally occurring amino acid

<400>  646

Met Ala Xaa Xaa Ala Xaa Xaa Leu Leu Ala Gly Xaa Xaa Xaa Ala Xaa
1                   5                   10                  15
Xaa Xaa Asp Pro Xaa Pro Xaa Xaa Ala Xaa Ala Xaa Xaa Pro Lys Xaa
                20                  25                  30
Ala Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Glu Ala Ile Xaa Xaa Xaa Xaa
        35                  40                  45
Xaa Leu Xaa Xaa Xaa Xaa Ala Xaa Ala Xaa Xaa Xaa Xaa Gln Xaa Xaa
    50                  55                  60
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Ala Xaa Xaa Xaa Xaa Xaa Leu Xaa
65                  70                  75                  80
Xaa Xaa Phe Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                85                  90                  95
Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Glu Xaa Xaa Xaa
            100                 105                 110
Ala Xaa Xaa Val Xaa Xaa Ala Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        115                 120                 125
Xaa Leu Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Tyr
    130                 135                 140
Xaa Xaa Xaa Xaa Thr Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Ile Xaa Xaa
145                 150                 155                 160
Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Val Xaa
            165                 170                 175
Xaa Asp Ala Leu Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa
            180                 185                 190
Xaa Met Xaa Xaa Xaa Ile Gly Gly Xaa Xaa Tyr Xaa Ile Ala Xaa Xaa
            195                 200                 205
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Ala
    210                 215                 220
Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa
225                 230                 235                 240
Xaa Xaa Ala Xaa Xaa Xaa Xaa Ser Xaa Ala Gly Xaa Xaa Xaa Xaa Ala
            245                 250                 255
Xaa Asp Xaa Ala Xaa Xaa Xaa Ser Xaa Ala Ala Xaa Xaa Xaa Xaa Xaa
            260                 265                 270
Xaa Xaa Xaa Xaa Asn Xaa Xaa Ala Asn Xaa Xaa Asn Tyr Ser Xaa Ala
        275                 280                 285
```

```
Arg Val Xaa Xaa Ala Xaa Xaa Xaa Ala Ala Xaa Xaa Xaa Ser Xaa Xaa
    290             295             300
Xaa Xaa Ser Xaa Ser Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
305             310             315                     320
Xaa Ala Xaa Xaa Xaa Ser Xaa Xaa Tyr Xaa Xaa Xaa Thr Xaa Xaa Xaa
            325             330                     335
Xaa Ile Xaa Xaa Thr Xaa Xaa Ala Xaa Pro Xaa Xaa Ala Gly Xaa Ala
            340             345             350
Xaa Leu Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa Thr Xaa Ala Xaa Xaa Ala
            355             360             365
Xaa Xaa Xaa Xaa Xaa Gly Xaa Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            370             375             380
Xaa Xaa Ala Xaa Xaa Xaa Xaa Leu Xaa Ser Xaa Xaa Ser Xaa Gly Ser
385             390             395                     400
Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser Cys Ser Xaa Tyr Xaa Xaa Ser Xaa
            405             410                     415
Ser Gly Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Gln Pro Asn Gly Ser
            420             425             430
Tyr Xaa Xaa Xaa Xaa Xaa Ala Gly Thr His Xaa Xaa Xaa Leu Xaa Gly
            435             440             445
Pro Ala Gly Xaa Asp Phe Asp Leu Tyr Leu Xaa Arg Trp Xaa Gly Ser
    450             455             460
Xaa Trp Leu Thr Val Ala Xaa Ser Thr Xaa Pro Xaa Ser Xaa Glu Ser
465             470             475                     480
Ile Ser Tyr Xaa Gly Xaa Ala Gly Tyr Tyr Xaa Trp Xaa Ile Xaa Ala
            485             490                     495
Xaa Ser Gly Ser Gly Xaa Tyr Xaa Xaa Xaa Leu Xaa Xaa Pro
            500             505             510


<210>   647
<211>   190
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   consensus sequence

<220>
<221>   VARIANT
<222>   (6)..(188)
<223>   Xaa can be any naturally occurring amino acid

<400>   647

Asp Val Ile Gly Gly Xaa Xaa Tyr Xaa Ile Xaa Xaa Xaa Xaa Arg Xaa
1               5               10              15
Xaa Xaa Xaa Xaa Cys Ser Ile Gly Phe Ala Val Xaa Gly Gly Phe Val
            20              25              30
Thr Ala Gly His Cys Gly Arg Xaa Gly Ala Xaa Xaa Xaa Xaa Xaa Xaa
            35              40              45
Thr Ser Xaa Pro Xaa Gly Thr Phe Xaa Gly Ser Ser Phe Pro Gly Asn
    50              55              60
Asp Tyr Ala Trp Val Gln Val Ala Ser Gly Asn Thr Pro Val Gly Ala
65              70              75                      80
Val Asn Asn Tyr Ser Gly Gly Thr Val Xaa Val Ala Gly Ser Thr Xaa
            85              90                      95
Ala Ala Val Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp
```

```
                      100                    105                    110
Arg Cys Gly Thr Ile Xaa Ala Tyr Asn Ala Ser Val Xaa Tyr Ala Glu
            115                    120                    125
Gly Thr Val Ser Gly Leu Ile Arg Thr Asn Val Cys Ala Glu Pro Gly
        130                    135                    140
Asp Ser Gly Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val Thr
145                    150                    155                    160
Ser Gly Gly Ser Gly Asn Cys Xaa Xaa Gly Gly Thr Thr Tyr Phe Gln
                165                    170                    175
Pro Val Asn Xaa Xaa Leu Xaa Xaa Tyr Gly Leu Xaa Leu Val
            180                    185                    190


<210>  648
<211>  368
<212>  PRT
<213>  Thermobifida fusca


<400>  648

Met Asn His Ser Ser Arg Arg Thr Thr Ser Leu Leu Phe Thr Ala Ala
1                   5                    10                    15
Leu Ala Ala Thr Ala Leu Val Ala Ala Thr Thr Pro Ala Ser Ala Gln
                20                    25                    30
Glu Leu Ala Leu Lys Arg Asp Leu Gly Leu Ser Asp Ala Glu Val Ala
            35                    40                    45
Glu Leu Arg Ala Ala Glu Ala Glu Ala Val Glu Leu Glu Glu Glu Leu
        50                    55                    60
Arg Asp Ser Leu Gly Ser Asp Phe Gly Gly Val Tyr Leu Asp Ala Asp
65                    70                    75                    80
Thr Thr Glu Ile Thr Val Ala Val Thr Asp Pro Ala Ala Val Ser Arg
                85                    90                    95
Val Asp Ala Asp Asp Val Thr Val Asp Val Val Asp Phe Gly Glu Thr
                100                    105                    110
Ala Leu Asn Asp Phe Val Ala Ser Leu Asn Ala Ile Ala Asp Thr Ala
            115                    120                    125
Asp Pro Lys Val Thr Gly Trp Tyr Thr Asp Leu Glu Ser Asp Ala Val
        130                    135                    140
Val Ile Thr Thr Leu Arg Gly Gly Thr Pro Ala Ala Glu Glu Leu Ala
145                    150                    155                    160
Glu Arg Ala Gly Leu Asp Glu Arg Ala Val Arg Ile Val Glu Glu Asp
                165                    170                    175
Glu Glu Pro Gln Ser Leu Ala Ala Ile Ile Gly Gly Asn Pro Tyr Tyr
                180                    185                    190
Phe Gly Asn Tyr Arg Cys Ser Ile Gly Phe Ser Val Arg Gln Gly Ser
            195                    200                    205
Gln Thr Gly Phe Ala Thr Ala Gly His Cys Gly Ser Thr Gly Thr Arg
        210                    215                    220
Val Ser Ser Pro Ser Gly Thr Val Ala Gly Ser Tyr Phe Pro Gly Arg
225                    230                    235                    240
Asp Met Gly Trp Val Arg Ile Thr Ser Ala Asp Thr Val Thr Pro Leu
                245                    250                    255
Val Asn Arg Tyr Asn Gly Gly Thr Val Thr Val Thr Gly Ser Gln Glu
                260                    265                    270
Ala Ala Thr Gly Ser Ser Val Cys Arg Ser Gly Ala Thr Thr Gly Trp
            275                    280                    285
Arg Cys Gly Thr Ile Gln Ser Lys Asn Gln Thr Val Arg Tyr Ala Glu
        290                    295                    300
```

```
Gly Thr Val Thr Gly Leu Thr Arg Thr Thr Ala Cys Ala Glu Gly Gly
305                 310                 315                 320
Asp Ser Gly Gly Pro Trp Leu Thr Gly Ser Gln Ala Gln Gly Val Thr
                325                 330                 335
Ser Gly Gly Thr Gly Asp Cys Arg Ser Gly Gly Ile Thr Phe Phe Gln
            340                 345                 350
Pro Ile Asn Pro Leu Leu Ser Tyr Phe Gly Leu Gln Leu Val Thr Gly
        355                 360                 365
```

<210> 649
<211> 382
<212> PRT
<213> Streptomyces spp.

<400> 649

```
Met Arg His Thr Gly Arg Asn Ala Ile Gly Ala Ala Ile Ala Ala Ser
1               5                   10                  15
Ala Leu Ala Phe Ala Leu Val Pro Ser Gln Ala Ala Ala Asn Asp Thr
            20                  25                  30
Leu Thr Glu Arg Ala Glu Ala Ala Val Ala Asp Leu Pro Ala Gly Val
        35                  40                  45
Leu Asp Ala Met Glu Arg Asp Leu Gly Leu Ser Glu Gln Glu Ala Gly
        50                  55                  60
Leu Lys Leu Val Ala Glu His Asp Ala Ala Leu Leu Gly Glu Thr Leu
65                  70                  75                  80
Ser Ala Asp Leu Asp Ala Phe Ala Gly Ser Trp Leu Ala Glu Gly Thr
                85                  90                  95
Glu Leu Val Val Ala Thr Thr Ser Glu Ala Glu Ala Ala Glu Ile Thr
            100                 105                 110
Glu Ala Gly Ala Thr Ala Glu Val Val Asp His Thr Leu Ala Glu Leu
        115                 120                 125
Asp Ser Val Lys Asp Ala Leu Asp Thr Ala Ala Glu Ser Tyr Asp Thr
        130                 135                 140
Thr Asp Ala Pro Val Trp Tyr Val Asp Val Thr Thr Asn Gly Val Val
145                 150                 155                 160
Leu Leu Thr Ser Asp Val Thr Glu Ala Glu Gly Phe Val Glu Ala Ala
                165                 170                 175
Gly Val Asn Ala Ala Ala Val Asp Ile Gln Thr Ser Asp Glu Gln Pro
            180                 185                 190
Gln Ala Phe Tyr Asp Leu Val Gly Gly Asp Ala Tyr Tyr Met Gly Gly
        195                 200                 205
Gly Arg Cys Ser Val Gly Phe Ser Val Thr Gln Gly Ser Thr Pro Gly
        210                 215                 220
Phe Ala Thr Ala Gly His Cys Gly Thr Val Gly Thr Ser Thr Thr Gly
225                 230                 235                 240
Tyr Asn Gln Ala Ala Gln Gly Thr Phe Glu Glu Ser Ser Phe Pro Gly
                245                 250                 255
Asp Asp Met Ala Trp Val Ser Val Asn Ser Asp Trp Asn Thr Thr Pro
            260                 265                 270
Thr Val Asn Glu Gly Glu Val Thr Val Ser Gly Ser Thr Glu Ala Ala
            275                 280                 285
Val Gly Ala Ser Ile Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys
        290                 295                 300
Gly Thr Ile Gln Gln His Asn Thr Ser Val Thr Tyr Pro Glu Gly Thr
305                 310                 315                 320
Ile Thr Gly Val Thr Arg Thr Ser Val Cys Ala Glu Pro Gly Asp Ser
```

```
                      325                     330                     335
Gly Gly Ser Tyr Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly
        340                     345                     350
Gly Ser Gly Asn Cys Thr Ser Gly Gly Thr Thr Tyr His Gln Pro Ile
        355                     360                     365
Asn Pro Leu Leu Ser Ala Tyr Gly Leu Asp Leu Val Thr Gly
    370                     375                     380


<210>  650
<211>  388
<212>  PRT
<213>  Streptomyces spp.


<400>  650

Met Arg Leu Lys Gly Arg Thr Val Ala Ile Gly Ser Ala Leu Ala Ala
1                   5                   10                  15
Ser Ala Leu Ala Leu Ser Leu Val Pro Ala Asn Ala Ser Ser Glu Leu
            20                  25                  30
Pro Ser Ala Glu Thr Ala Lys Ala Asp Ala Leu Val Glu Gln Leu Pro
        35                  40                  45
Ala Gly Met Val Asp Ala Met Glu Arg Asp Leu Gly Val Pro Ala Ala
    50                  55                  60
Glu Val Gly Asn Gln Leu Val Ala Glu His Glu Ala Ala Val Leu Glu
65                  70                  75                  80
Glu Ser Leu Ser Glu Asp Leu Ser Gly Tyr Ala Gly Ser Trp Ile Val
            85                  90                  95
Glu Gly Thr Ser Glu His Val Val Ala Thr Thr Asp Arg Ala Glu Ala
            100                 105                 110
Ala Glu Ile Thr Ala Ala Gly Ala Thr Ala Thr Val Val Glu His Ser
        115                 120                 125
Leu Ala Glu Leu Glu Ala Val Lys Asp Ile Leu Asp Glu Ala Ala Thr
    130                 135                 140
Ala Asn Pro Glu Asp Ala Ala Pro Val Trp Tyr Val Asp Val Thr Thr
145                 150                 155                 160
Asn Glu Val Val Val Leu Ala Ser Asp Val Pro Ala Ala Glu Ala Phe
            165                 170                 175
Val Ala Ala Ser Gly Ala Asp Ala Ser Thr Val Arg Val Glu Arg Ser
            180                 185                 190
Asp Glu Ser Pro Gln Pro Phe Tyr Asp Leu Val Gly Gly Asp Ala Tyr
        195                 200                 205
Tyr Ile Gly Asn Gly Arg Cys Ser Ile Gly Phe Ser Val Arg Gln Gly
    210                 215                 220
Ser Thr Pro Gly Phe Val Thr Ala Gly His Cys Gly Ser Val Gly Asn
225                 230                 235                 240
Ala Thr Thr Gly Phe Asn Arg Val Ser Gln Gly Thr Phe Arg Gly Ser
            245                 250                 255
Trp Phe Pro Gly Arg Asp Met Ala Trp Val Ala Val Asn Ser Asn Trp
            260                 265                 270
Thr Pro Thr Ser Leu Val Arg Asn Ser Gly Ser Gly Val Arg Val Thr
        275                 280                 285
Gly Ser Thr Gln Ala Thr Val Gly Ser Ser Ile Cys Arg Ser Gly Ser
    290                 295                 300
Thr Thr Gly Trp Arg Cys Gly Thr Ile Gln Gln His Asn Thr Ser Val
305                 310                 315                 320
Thr Tyr Pro Gln Gly Thr Ile Thr Gly Val Thr Arg Thr Ser Ala Cys
            325                 330                 335
```

```
Ala Gln Pro Gly Asp Ser Gly Gly Ser Phe Ile Ser Gly Thr Gln Ala
        340                 345                 350
Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Ser Ile Gly Gly Thr
        355         .           360                 365
Thr Phe His Gln Pro Val Asn Pro Ile Leu Ser Gln Tyr Gly Leu Thr
    370                 375                 380
Leu Val Arg Ser
385


<210>   651
<211>   .458
<212>   PRT
<213>   Streptomyces lividans


<400>   651

Met Val Gly Arg His Ala Ala Arg Ser Arg Arg Ala Ala Leu Thr Ala
1            .    5                 10                  15
Leu Gly Ala Leu Val Leu Thr Ala Leu Pro Ser Ala Ala Ser Ala Ala
            20                  25                  30          .
Pro Pro Pro Val Pro Gly Pro Arg Pro Ala Val Ala Arg Thr Pro Asp
        35                  40                  45
Ala Ala Thr Ala Pro Ala Arg Met Leu Ser Ala Met Glu Arg Asp Leu
    50                  55                  60
Arg Leu Ala Pro Gly Gln Ala Ala Ala Arg Pro Val Asn Glu Ala Glu
65                  70                  75                  80
Ala Gly Thr Arg Ala Gly Met Leu Arg Asn Thr Leu Gly Asp Arg Phe
            85                  90                  95
Ala Gly Ala Trp Val Ser Gly Ala Thr Ser Ala Glu Leu Thr Val Ala
            100                 105                 110
Thr Thr Asp Ala Ala Asp Thr Ala Ala Ile Glu Ala Gln Gly Ala Lys
        115                 120                 125
Ala Ala Val Val Gly Arg Asn Leu Ala Glu Leu Arg Ala Val Lys Glu
    130                 135                 140
Lys Leu Asp Ala Ala Ala Val Arg Thr Arg Thr Arg Gln Thr Pro Val
145                 150                 155                 160
Trp Tyr Val Asp Val Lys Thr Asn Arg Val Thr Val Gln Ala Thr Gly
            165                 170                 175
Ala Ser Ala Ala Ala Ala Phe Val Glu Ala Ala Gly Val Pro Ala Ala
            180                 185                 190
Asp Val Gly Val Arg Val Ser Pro Asp Gln Pro Arg Val Leu Glu Asp
        195                 200                 205
Leu Val Gly Gly Asp Ala Tyr Tyr Ile Asp Asp Gln Ala Arg Cys Ser
    210                 215                 220
Ile Gly Phe Ser Val Thr Lys Asp Asp Gln Glu Gly Phe Ala Thr Ala
225                 230                 235                 240
Gly His Cys Gly Asp Pro Gly Ala Thr Thr Thr Gly Tyr Asn Glu Ala
            245                 250                 255
Asp Gln Gly Thr Phe Gln Ala Ser Thr Phe Pro Gly Lys Asp Met Ala
            260                 265                 270
Trp Val Gly Val Asn Ser Asp Trp Thr Ala Thr Pro Asp Val Lys Ala
            275                 280                 285
Glu Gly Gly Glu Lys Ile Gln Leu Ala Gly Ser Val Glu Ala Leu Val
    290                 295                 300
Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly
305                 310                 315                 320
Thr Ile Gln Gln His Asp Thr Ser Val Thr Tyr Pro Glu Gly Thr Val
```

```
                        325                     330                     335
Asp Gly Leu Thr Gly Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
            340                     345                     350
Gly Pro Phe Val Ser Gly Val Gln Ala Gln Gly Thr Thr Ser Gly Gly
            355                     360                     365
Ser Gly Asp Cys Thr Asn Gly Gly Thr Thr Phe Tyr Gln Pro Val Asn
            370                     375                     380
Pro Leu Leu Ser Asp Phe Gly Leu Thr Leu Lys Thr Thr Ser Ala Ala
385                     390                     395                     400
Thr Gln Thr Pro Ala Pro Gln Asp Asn Ala Ala Ala Asp Ala Trp Thr
            405                     410                     415
Ala Gly Arg Val Tyr Glu Val Gly Thr Thr Val Ser Tyr Asp Gly Val
            420                     425                     430
Arg Tyr Arg Cys Leu Gln Ser His Gln Ala Gln Gly Val Gly Ser Pro
            435                     440                     445
Ala Ser Val Pro Ala Leu Trp Gln Arg Val
            450                     455
```

<210> 652
<211> 458
<212> PRT
<213> Streptomyces coelicolor A3(2)

<400> 652

```
Met Val Gly Arg His Ala Ala Arg Ser Arg Arg Ala Ala Leu Thr Ala
1                   5                   10                  15
Leu Gly Ala Leu Val Leu Thr Ala Leu Pro Ser Ala Ala Ser Ala Ala
            20                      25                      30
Pro Pro Pro Val Pro Gly Pro Arg Pro Ala Val Ala Arg Thr Pro Asp
            35                      40                      45
Ala Ala Thr Ala Pro Ala Arg Met Leu Ser Ala Met Glu Arg Asp Leu
            50                      55                      60
Arg Leu Ala Pro Gly Gln Ala Ala Ala Arg Leu Val Asn Glu Ala Glu
65                      70                      75                      80
Ala Gly Thr Arg Ala Gly Met Leu Arg Asn Thr Leu Gly Asp Arg Phe
            85                      90                      95
Ala Gly Ala Trp Val Ser Gly Ala Thr Ser Ala Glu Leu Thr Val Ala
            100                     105                     110
Thr Thr Asp Ala Ala Asp Thr Ala Ala Ile Glu Ala Gln Gly Ala Lys
            115                     120                     125
Ala Ala Val Val Gly Arg Asn Leu Ala Glu Leu Arg Ala Val Lys Glu
            130                     135                     140
Lys Leu Asp Ala Ala Ala Val Arg Thr Arg Thr Arg Gln Thr Pro Val
145                     150                     155                     160
Trp Tyr Val Asp Val Lys Thr Asn Arg Val Thr Val Gln Ala Thr Gly
            165                     170                     175
Ala Ser Ala Ala Ala Ala Phe Val Glu Ala Ala Gly Val Pro Ala Ala
            180                     185                     190
Asp Val Gly Val Arg Val Ser Pro Asp Gln Pro Arg Val Leu Glu Asp
            195                     200                     205
Leu Val Gly Gly Asp Ala Tyr Tyr Ile Asp Asp Gln Ala Arg Cys Ser
            210                     215                     220
Ile Gly Phe Ser Val Thr Lys Asp Asp Gln Glu Gly Phe Ala Thr Ala
225                     230                     235                     240
Gly His Cys Gly Asp Pro Gly Ala Thr Thr Thr Gly Tyr Asn Glu Ala
            245                     250                     255
```

```
Asp Gln Gly Thr Phe Gln Ala Ser Thr Phe Pro Gly Lys Asp Met Ala
        260             265             270
Trp Val Gly Val Asn Ser Asp Trp Thr Ala Thr Pro Asp Val Lys Ala
        275             280             285
Glu Gly Gly Glu Lys Ile Gln Leu Ala Gly Ser Val Glu Ala Leu Val
        290             295             300
Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly
305             310             315             320
Thr Ile Gln Gln His Asp Thr Ser Val Thr Tyr Pro Glu Gly Thr Val
                325             330             335
Asp Gly Leu Thr Glu Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
        340             345             350
Gly Pro Phe Val Ser Gly Val Gln Ala Gln Gly Thr Thr Ser Gly Gly
        355             360             365
Ser Gly Asp Cys Thr Asn Gly Gly Thr Thr Phe Tyr Gln Pro Val Asn
        370             375             380
Pro Leu Leu Ser Asp Phe Gly Leu Thr Leu Lys Thr Thr Ser Ala Ala
385             390             395             400
Thr Gln Thr Pro Ala Pro Gln Asp Asn Ala Ala Ala Asp Ala Trp Thr
                405             410             415
Ala Gly Arg Val Tyr Glu Val Gly Thr Thr Val Ser Tyr Asp Gly Val
                420             425             430
Arg Tyr Arg Cys Leu Gln Ser His Gln Ala Gln Gly Val Gly Ser Pro
        435             440             445
Ala Ser Val Pro Ala Leu Trp Gln Arg Val
        450             455
```

```
<210>   653
<211>   456
<212>   PRT
<213>   Streptomyces avermitilis MA-4680

<400>   653
```

```
Met Val His Arg His Val Gly Ala Gly Cys Ala Gly Leu Ser Val Leu
1               5               10              15
Ala Thr Leu Val Leu Thr Gly Leu Pro Ala Ala Ala Ile Glu Pro
        20              25              30
Pro Gly Pro Ala Pro Ala Pro Ser Ala Val Gln Pro Leu Gly Ala Gly
        35              40              45
Asn Pro Ser Thr Ala Val Leu Gly Ala Leu Gln Arg Asp Leu His Leu
        50              55              60
Thr Asp Thr Gln Ala Lys Thr Arg Leu Val Asn Glu Met Glu Ala Gly
65              70              75              80
Thr Arg Ala Gly Arg Leu Gln Asn Ala Leu Gly Lys His Phe Ala Gly
                85              90              95
Ala Trp Val His Gly Ala Ala Ser Ala Asp Leu Thr Val Ala Thr Thr
                100             105             110
His Ala Thr Asp Ile Pro Ala Ile Thr Ala Gly Gly Ala Thr Ala Val
        115             120             125
Val Val Lys Thr Gly Leu Asp Asp Leu Lys Gly Ala Lys Lys Lys Leu
        130             135             140
Asp Ser Ala Val Ala His Gly Gly Thr Ala Val Asn Thr Pro Val Arg
145             150             155             160
Tyr Val Asp Val Arg Thr Asn Arg Val Thr Leu Gln Ala Arg Ser Arg
                165             170             175
Ala Ala Ala Asp Ala Leu Ile Ala Ala Ala Gly Val Asp Ser Gly Leu
```

```
              180                      185                      190
Val Asp Val Lys Val Ser Glu Asp Arg Pro Arg Ala Leu Phe Asp Ile
         195                      200                      205
Arg Gly Gly Asp Ala Tyr Tyr Ile Asp Asn Thr Ala Arg Cys Ser Val
    210                      215                      220
Gly Phe Ser Val Thr Lys Gly Asn Gln Gln Gly Phe Ala Thr Ala Gly
225                      230                      235                      240
His Cys Gly Arg Ala Gly Ala Pro Thr Ala Gly Phe Asn Glu Val Ala
                 245                      250                      255
Gln Gly Thr Val Gln Ala Ser Val Phe Pro Gly His Asp Met Ala Trp
             260                      265                      270
Val Gly Val Asn Ser Asp Trp Thr Ala Thr Pro Asp Val Ala Gly Ala
         275                      280                      285
Ala Gly Gln Asn Val Ser Ile Ala Gly Ser Val Gln Ala Ile Val Gly
    290                      295                      300
Ala Ala Ile Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr
305                      310                      315                      320
Val Glu Glu His Asp Thr Ser Val Thr Tyr Glu Glu Gly Thr Val Asp
                 325                      330                      335
Gly Leu Thr Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Gly
             340                      345                      350
Ser Phe Val Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Ser
         355                      360                      365
Gly Asp Cys Thr Arg Gly Gly Thr Thr Tyr Tyr Gln Pro Val Asn Pro
    370                      375                      380
Ile Leu Ser Thr Tyr Gly Leu Thr Leu Lys Thr Ser Thr Ala Pro Thr
385                      390                      395                      400
Asp Thr Pro Ser Asp Pro Val Asp Gln Ser Gly Val Trp Ala Ala Gly
             405                      410                      415
Arg Val Tyr Glu Val Gly Ala Gln Val Thr Tyr Ala Gly Val Thr Tyr
         420                      425                      430
Gln Cys Leu Gln Ser His Gln Ala Gln Gly Val Trp Gln Pro Ala Ala
             435                      440                      445
Thr Pro Ala Leu Trp Gln Arg Leu
    450                      455


<210>   654
<211>   458
<212>   PRT
<213>   Streptomyces lividans


<400>   654

Met Pro His Arg His Arg His His Arg Ala Val Gly Ala Ala Val Ala
1                 5                       10                      15
Ala Thr Ala Ala Leu Leu Val Ala Gly Leu Ser Gly Ser Ala Ser Ala
             20                      25                      30
Gly Thr Ala Pro Ala Gly Ser Ala Pro Thr Ala Ala Glu Thr Leu Arg
         35                      40                      45
Thr Asp Ala Ala Pro Pro Ala Leu Leu Lys Ala Met Gln Arg Asp Leu
    50                      55                      60
Gly Ile Asp Arg Arg Gln Ala Glu Arg Arg Leu Val Asn Glu Ala Glu
65                      70                      75                      80
Ala Gly Ala Thr Ala Gly Arg Leu Arg Ala Ala Leu Gly Gly Asp Phe
                 85                      90                      95
Ala Gly Ala Trp Val Arg Gly Ala Glu Ser Gly Thr Leu Thr Val Ala
             100                     105                     110
```

```
Thr Thr Asp Ala Gly Asp Val Ala Ala Val Glu Ala Arg Gly Ala Glu
        115                 120                 125
Ala Lys Val Val Arg His Ser Leu Ala Asp Leu Asp Ala Ala Lys Ala
    130                 135                 140
Arg Leu Asp Thr Ala Ala Ala Gly Leu Asn Thr Ala Asp Ala Pro Val
145                 150                 155                 160
Trp Tyr Val Asp Thr Arg Thr Asn Thr Val Val Val Glu Ala Ile Arg
            165                 170                 175
Pro Ala Ala Ala Arg Ser Leu Leu Thr Ala Ala Gly Val Asp Gly Ser
        180                 185                 190
Leu Ala His Val Lys Asn Arg Thr Glu Arg Pro Arg Thr Phe Tyr Asp
        195                 200                 205
Leu Arg Gly Gly Glu Ala Tyr Tyr Ile Asn Asn Ser Ser Arg Cys Ser
    210                 215                 220
Ile Gly Phe Pro Ile Thr Lys Gly Thr Gln Gln Gly Phe Ala Thr Ala
225                 230                 235                 240
Gly His Cys Asp Arg Ala Gly Ser Ser Thr Thr Gly Ala Asn Arg Val
            245                 250                 255
Ala Gln Gly Thr Phe Gln Gly Ser Ile Phe Pro Gly Arg Asp Met Ala
        260                 265                 270
Trp Val Ala Thr Asn Ser Ser Trp Thr Ala Thr Pro Tyr Val Leu Gly
        275                 280                 285
Ala Gly Gly Gln Asn Val Gln Val Thr Gly Ser Thr Ala Ser Pro Val
    290                 295                 300
Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly
305                 310                 315                 320
Thr Val Thr Gln Leu Asn Thr Ser Val Thr Tyr Gln Glu Gly Thr Ile
            325                 330                 335
Ser Pro Val Thr Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
            340                 345                 350
Gly Ser Phe Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly
    355                 360                 365
Ser Gly Asp Cys Arg Thr Gly Gly Gly Thr Phe Phe Gln Pro Ile Asn
    370                 375                 380
Ala Leu Leu Gln Asn Tyr Gly Leu Thr Leu Lys Thr Thr Gly Gly Asp
385                 390                 395                 400
Asp Gly Gly Gly Asp Asp Gly Gly Glu Glu Pro Gly Gly Thr Trp Ala
            405                 410                 415
Ala Gly Thr Val Tyr Gln Pro Gly Asp Thr Val Thr Tyr Gly Gly Ala
            420                 425                 430
Thr Phe Arg Cys Leu Gln Gly His Gln Ala Tyr Ala Gly Trp Glu Pro
        435                 440                 445
Pro Asn Val Pro Ala Leu Trp Gln Arg Val
    450                 455
```

<210> 655
<211> 463
<212> PRT
<213> Streptomyces coelicolor A3(2)

<400> 655

```
Met Pro His Arg His Arg His His Arg Ala Val Gly Ala Ala Val Ala
1               5                   10                  15
Ala Thr Ala Ala Leu Leu Val Ala Gly Leu Ser Gly Ser Ala Ser Ala
            20                  25                  30
Gly Thr Ala Pro Ala Gly Ser Ala Pro Thr Ala Ala Glu Thr Leu Arg
```

```
              35                      40                      45
Thr Asp Ala Ala Pro Pro Ala Leu Leu Lys Ala Met Gln Arg Asp Leu
    50                      55                      60
Gly Leu Asp Arg Arg Gln Ala Glu Arg Arg Leu Val Asn Glu Ala Glu
65                      70                      75                      80
Ala Gly Ala Thr Ala Gly Arg Leu Arg Ala Ala Leu Gly Gly Asp Phe
                85                      90                      95
Ala Gly Ala Trp Val Arg Gly Ala Glu Ser Gly Thr Leu Thr Val Ala
                100                     105                     110
Thr Thr Asp Ala Gly Asp Val Ala Ala Ile Glu Ala Arg Gly Ala Glu
                115                     120                     125
Ala Lys Val Val Arg His Ser Leu Ala Asp Leu Asp Ala Ala Lys Ala
        130                     135                     140
Arg Leu Asp Thr Ala Ala Ala Gly Leu Asn Thr Ala Asp Ala Pro Val
145                     150                     155                     160
Trp Tyr Val Asp Thr Arg Thr Asn Thr Val Val Val Glu Ala Ile Arg
                165                     170                     175
Pro Ala Ala Ala Arg Ser Leu Leu Thr Ala Ala Gly Val Asp Gly Ser
                180                     185                     190
Leu Ala His Val Lys Asn Arg Thr Glu Arg Pro Arg Thr Phe Tyr Asp
                195                     200                     205
Leu Arg Gly Gly Glu Ala Tyr Tyr Ile Asn Asn Ser Ser Arg Cys Ser
        210                     215                     220
Ile Gly Phe Pro Ile Thr Lys Gly Thr Gln Gln Gly Phe Ala Thr Ala
225                     230                     235                     240
Gly His Cys Gly Arg Ala Gly Ser Ser Thr Thr Gly Ala Asn Arg Val
                245                     250                     255
Ala Gln Gly Thr Phe Gln Gly Ser Ile Phe Pro Gly Arg Asp Met Ala
                260                     265                     270
Trp Val Ala Thr Asn Ser Ser Trp Thr Ala Thr Pro Tyr Val Leu Gly
        275                     280                     285
Ala Gly Gly Gln Asn Val Gln Val Thr Gly Ser Thr Ala Ser Pro Val
        290                     295                     300
Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly
305                     310                     315                     320
Thr Val Thr Gln Leu Asn Thr Ser Val Thr Tyr Gln Glu Gly Thr Ile
                325                     330                     335
Ser Pro Val Thr Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
        340                     345                     350
Gly Ser Phe Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly
        355                     360                     365
Ser Gly Asp Cys Arg Thr Gly Gly Glu Thr Phe Phe Gln Pro Ile Asn
        370                     375                     380
Ala Leu Leu Gln Asn Tyr Gly Leu Thr Leu Lys Thr Thr Gly Gly Asp
385                     390                     395                     400
Asp Gly Gly Gly Asp Asp Gly Gly Gly Asp Asp Gly Gly Glu Glu Pro
                405                     410                     415
Gly Gly Thr Trp Ala Ala Gly Thr Val Tyr Gln Pro Gly Asp Thr Val
                420                     425                     430
Thr Tyr Gly Gly Ala Thr Phe Arg Cys Leu Gln Gly His Gln Ala Tyr
        435                     440                     445
Ala Gly Trp Glu Pro Pro Asn Val Pro Ala Leu Trp Gln Arg Val
    450                     455                     460

<210>  656
<211>  457
<212>  PRT
```

<213> Streptomyces griseus

<400> 656

```
Met Glu Arg Thr Thr Leu Arg Arg Arg Ala Leu Val Ala Gly Thr Ala
1               5                   10                  15
Thr Val Ala Val Gly Ala Leu Ala Leu Ala Gly Leu Thr Gly Val Ala
            20                  25                  30
Ser Ala Asp Pro Ala Ala Thr Ala Ala Pro Pro Val Ser Ala Asp Ser
            35                  40                  45
Leu Ser Pro Gly Met Leu Ala Ala Leu Glu Arg Asp Leu Gly Leu Asp
    50                  55                  60
Glu Asp Ala Ala Arg Ser Arg Ile Ala Asn Glu Tyr Arg Ala Ala Ala
65                  70                  75                  80
Val Ala Ala Gly Leu Glu Lys Ser Leu Gly Ala Arg Tyr Ala Gly Ala
            85                  90                  95
Arg Val Ser Gly Ala Lys Ala Thr Leu Thr Val Ala Thr Thr Asp Ala
            100                 105                 110
Ser Glu Ala Ala Arg Ile Thr Glu Ala Gly Ala Arg Ala Glu Val Val
            115                 120                 125
Gly His Ser Leu Asp Arg Phe Glu Gly Val Lys Lys Ser Leu Asp Lys
    130                 135                 140
Ala Ala Leu Asp Lys Ala Pro Lys Asn Val Pro Val Trp Tyr Val Asp
145                 150                 155                 160
Val Ala Ala Asn Arg Val Val Val Asn Ala Ala Ser Pro Ala Ala Gly
            165                 170                 175
Gln Ala Phe Leu Lys Val Ala Gly Val Asp Arg Gly Leu Val Thr Val
            180                 185                 190
Ala Arg Ser Ala Glu Gln Pro Arg Ala Leu Ala Asp Ile Arg Gly Gly
            195                 200                 205
Asp Ala Tyr Tyr Met Asn Gly Ser Gly Arg Cys Ser Val Gly Phe Ser
    210                 215                 220
Val Thr Arg Gly Thr Gln Asn Gly Phe Ala Thr Ala Gly His Cys Gly
225                 230                 235                 240
Arg Val Gly Thr Thr Thr Asn Gly Val Asn Gln Gln Ala Gln Gly Thr
            245                 250                 255
Phe Gln Gly Ser Thr Phe Pro Gly Arg Asp Ile Ala Trp Val Ala Thr
            260                 265                 270
Asn Ala Asn Trp Thr Pro Arg Pro Leu Val Asn Gly Tyr Gly Arg Gly
    275                 280                 285
Asp Val Thr Val Ala Gly Ser Thr Ala Ser Val Val Gly Ala Ser Val
    290                 295                 300
Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Gln Gln
305                 310                 315                 320
Leu Asn Thr Ser Val Thr Tyr Pro Glu Gly Thr Ile Ser Gly Val Thr
            325                 330                 335
Arg Thr Ser Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Tyr Ile
            340                 345                 350
Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys
    355                 360                 365
Ser Ser Gly Gly Thr Thr Tyr Phe Gln Pro Ile Asn Pro Leu Leu Gln
    370                 375                 380
Ala Tyr Gly Leu Thr Leu Val Thr Ser Gly Gly Gly Thr Pro Thr Asp
385                 390                 395                 400
Pro Pro Thr Thr Pro Pro Thr Asp Ser Pro Gly Gly Thr Trp Ala Val
            405                 410                 415
Gly Thr Ala Tyr Ala Ala Gly Ala Thr Val Thr Tyr Gly Gly Ala Thr
```

```
                    420                     425                     430
Tyr Arg Cys Leu Gln Ala His Thr Ala Gln Pro Gly Trp Thr Pro Ala
        435                     440                     445
Asp Val Pro Ala Leu Trp Gln Arg Val
    450                     455
```